

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 13:24:17 ; Search time 154 Seconds
(without alignments)
333.106 Million cell updates/sec

Title: US-09-913-569B-6
Perfect score: 756
Sequence: 1 MVHGTIEVLLVGAKGLENTD.....PEDTRQGLPEDFGWKQSS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	100.0	143	3 AAB44496	Aab44496 Plant vir
2	672	88.9	130	3 AAB44511	Aab44511 Plant vir
3	580.5	76.8	144	7 ADC53922	Adc53922 Rice phlo
4	575.5	76.1	144	3 AAB44498	Aab44498 Plant vir
5	523	69.2	129	3 AAB44495	Aab44495 Plant vir
6	523	69.2	145	6 AAE35936	Aae35936 Lolium pe
7	493	65.2	128	6 AAE35945	Aae35945 Lolium pe
8	483.5	64.0	147	3 AAG15489	Aag15489 Arabidops
9	470.5	62.2	202	3 AAB44510	Aab44510 Plant vir
10	459	60.7	130	3 AAB44494	Aab44494 Plant vir
11	454.5	60.1	145	3 AAB44507	Aab44507 Plant vir
12	445	58.9	140	3 AAB44497	Aab44497 Plant vir
13	429.5	56.8	142	3 AAB44509	Aab44509 Plant vir
14	419.5	55.5	133	3 AAG15297	Aag15297 Arabidops
15	404.5	53.5	149	3 AAB44508	Aab44508 Plant vir
16	398.5	52.7	123	3 AAG15490	Aag15490 Arabidops
17	368	48.7	107	3 AAB44512	Aab44512 Plant vir
18	328.5	43.5	102	3 AAG15298	Aag15298 Arabidops
19	325.5	43.1	102	3 AAG15491	Aag15491 Arabidops
20	278.5	36.8	157	3 AAB44501	Aab44501 Plant vir
21	271.5	35.9	151	3 AAB44504	Aab44504 Plant vir
22	260.5	34.5	154	3 AAB44505	Aab44505 Plant vir
23	260	34.4	154	3 AAB44503	Aab44503 Plant vir
24	249	32.9	156	7 ADC53926	Adc53926 Rice phlo
25	246	32.5	69	3 AAB44518	Aab44518 Plant vir

26	240.5	31.8	156	3 AAG54087	Aag54087 Arabidops
27	240.5	31.8	156	3 AAG11288	Aag11288 Arabidops
28	240.5	31.8	185	3 AAG54086	Aag54086 Arabidops
29	240.5	31.8	189	3 AAG11287	Aag11287 Arabidops
30	240.5	31.8	197	3 AAG23591	Aag23591 Arabidops
31	237.5	31.4	159	7 ADC53924	Adc53924 Rice phlo
32	220	29.1	102	3 AAB44502	Aab44502 Plant vir
33	205	27.1	89	3 AAB44515	Aab44515 Plant vir
34	175	23.1	85	3 AAB44514	Aab44514 Plant vir
35	166	22.0	244	3 AAG40015	Aag40015 Arabidops
36	166	22.0	245	3 AAG38059	Aag38059 Arabidops
37	166	22.0	245	3 AAG05889	Aag05889 Arabidops
38	166	22.0	247	3 AAG38058	Aag38058 Arabidops
39	166	22.0	247	3 AAG05888	Aag05888 Arabidops
40	166	22.0	263	3 AAG38057	Aag38057 Arabidops
41	166	22.0	274	3 AAG05887	Aag05887 Arabidops
42	156	20.6	99	3 AAB44516	Aab44516 Plant vir
43	150	19.8	258	3 AAB44500	Aab44500 Plant vir
44	127	16.8	308	3 AAB44499	Aab44499 Plant vir
45	125.5	16.6	466	4 AAB93562	Aab93562 Human pro

ALIGNMENTS

RESULT 1
AAB44496
ID AAB44496 standard; protein; 143 AA.
XX AAB44496;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 6.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Zea mays.
XX
PN WQ200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
(DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79350.
XX
PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 36-37; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes

CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 756; DB 3; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.3e-79;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVVGAKGLENTDYLGNMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

Db 1 MVHGTLEVLVVGAKGLENTDYLGNMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

Db 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

QY 121 TFTPEDTRQRLPEDFGWKQSS 143

Db 121 TFTPEDTRQRLPEDFGWKQSS 143

RESULT 2

AAB44511

ID AAB44511 standard; protein; 130 AA.

AC AAB44511;

XX

XX 06-FEB-2001 (first entry)

DT

XX

DE Plant viral movement protein SEQ ID 36.

XX

KW Plant viral movement protein; transport; transgenic plant;

KW viral resistance; cosuppression.

XX

OS Zea mays.

XX

PN WC2000060088-A2.

XX

PD 12-OCT-2000.

XX

PF 06-APR-2000; 2000WO-US0009110.

XX

PR 07-APR-1999; 99US-0128092P.

XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA

XX

PI Krebbers E, Weng Z, Cahoon RE;

XX

XX WPI; 2000-638467/61.

DR N-PSDB; AAC79365.

DR

XX

XX Novel viral movement polypeptides and polynucleotides useful in field of

PT plant molecular biology, for producing transgenic plants, to prepare

PT antibodies and in immunological screening of cDNA expression libraries.

XX

PS Claim 23; Page 53-54; 62pp; English.

XX

CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement

CC proteins AAB44494-B44520. Some plant viruses have been shown to be able

CC to establish systemic infections via movement proteins that utilize

CC existing plant pathways to traffic macromolecules to surrounding cells.

CC Proteins such as those of the invention are similar to viral movement

CC proteins that function in the transport of nucleic acids from cell to

CC cell. The plant viral movement proteins are useful for obtaining a

CC nucleic acid fragment encoding a viral movement protein. Polynucleotides

CC encoding the plant viral movement proteins are useful for positive

CC selection of a transformed cell. The proteins are useful in the field of

CC plant molecular biology, and in the preparation of antibodies against the

CC proteins. The proteins are also useful for isolating cDNAs and genes

CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 130 AA;

Query Match 88.9%; Score 672; DB 3; Length 130;
Best Local Similarity 98.5%; Pred. No. 1.2e-69;
Matches 128; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVVGAKGLENTDYLGNMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

Db 1 MVHGTLEVLVVGAKGLENTDYLGNMDPYAILKCRSQEQKSSIAIGKGTTPWNNENFIPTV 60

QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

Db 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCYGKIKVGL 120

QY 121 TFTPEDTRQR 130

Db 121 TFTPEDTRKR 130

RESULT 3

ADC53922

ID ADC53922 standard; protein; 144 AA.

XX

AC ADC53922;

XX

DT 18-DEC-2003 (first entry)

XX

DE Rice phloem protein of the invention #1.

XX

KW Rice; phloem protein; Ca2+/phospholipid-combining domain; promoter;

KW transgenic plant; phloem-specific; exotic protein; virus MP-like gene.

XX

OS Oryza sativa.

XX

PH Key Location/Qualifiers

FT Misc-difference 21 /note= "Encoded by TAC"

FT Misc-difference 28 /note= "Encoded by TAC"

FT Misc-difference 94 /note= "Encoded by TAT"

FT Misc-difference 104 /note= "Encoded by TAT"

FT Misc-difference 112 /note= "Encoded by TAC"

XX

XX JP2002315582-A.

PN

XX

XX 29-OCT-2002.

XX

PF 24-APR-2001; 2001JP-00126682.

XX

PR 24-APR-2001; 2001JP-00126682.

XX

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX

XX WPI; 2003-407228/39.

DR N-PSDB; ADC53921.

XX

PT A new protein in rice phloem and its gene, a DNA, a promotor, a

PT transgenic plant.

XX

PS Claim 3; SEQ ID NO 2; 18pp; Japanese.

XX

CC The invention discloses a rice phloem protein having Ca2+/phospholipid-

CC combining domain. Also claimed is a DNA encoding the novel rice phloem

CC protein, a promoter comprising a 1288 or 1572 base pair sequence, given

CC

CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 129 AA;

Query Match 69.2%; Score 523; DB 3; Length 129;
Best Local Similarity 78.6%; Pred. No. 2.4e-52;
Matches 99; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSIATGKTTPEWNNETFTV 60
Db 1 MAQGTLEVLVGAAGLENTDYLNNMDPYALQCRSHQKSSVAGKCEPEWNETFTV 60

QY 61 SDRTDVLVIMQSDTGTDADFVGEATIPLEAVVTERSIPPTLYNVVKGKCYGKIKVGL 120
Db 61 SDGAELFIKLLSDGTDGTDADFVGEATIPLEAVVTEGNIPTTYNVVKGKCYGKIKVGL 120

QY 121 TFTPED 126
Db 121 TFTPED 126

RESULT 6
AAE35936
ID AAE35936 standard; protein; 145 AA.
XX
AC AAE35936;
XX
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra) protein.
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipest;
KW agricultural; LpEra.
XX
OS Lolium perenne.
XX WO200288359-A1.
XX
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX

PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
XX
DR WPI; 2003-201227/19.
DR N-PSDB; AAD54386.
XX
PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 18; Fig 17; 195pp; English.

XX The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC

CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC protein
XX
SQ Sequence 145 AA;

Query Match 69.2%; Score 523; DB 6; Length 145;
Best Local Similarity 69.6%; Pred. No. 2.9e-52;
Matches 96; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 4 GTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSIATGKTTPEWNNETFTVSDR 63
Db 5 GTLEVLVGAAGLENTDYLNNMDPYALLVTSNEQRSSVAEGKSEPEWNETFTVTSN 64

QY 64 TTDLVIMKMSDGTGTDADFVGEATIPLEAVVTERSIPPTLYNVVKGKCYGKIKVGLTFT 123
Db 65 ATELCIKLLDDDDGTDGVARIPLDVYTEGSIPTTYNVVKGKCYGKIRIGLKFT 124

QY 124 PEDTRQGLPEDFGWKQ 141
Db 125 PEEYHLLPEENFGWRQ 142

RESULT 7
AAE35945
ID AAE35945 standard; protein; 128 AA.
XX
AC AAE35945;
XX
DT 17-JUN-2003 (first entry)
XX
DE Lolium perenne elicitor-responsive protein a (LpEra).
XX
KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
KW elicitor-responsive protein; disease resistance; plant defence response;
KW protein storage; pest resistance; genetic marker; gene therapy; antipest;
KW agricultural; LpEra.
XX
OS Lolium perenne.
XX WO200288359-A1.
XX
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-AU000539.
XX
XX
PR 02-MAY-2001; 2001AU-00004735.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX

PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
XX
DR WPI; 2003-201227/19.
DR N-PSDB; AAD54408.
XX
PT New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
PT elicitor-responsive or defensin polypeptide, for modifying disease and/or
PT plant resistance, plant defence response and/or protein storage in a
PT plant.
XX
PS Claim 18; Fig 50; 195pp; English.

XX The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
CC nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
CC responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
CC such proteins. Sequences of the invention are useful to modify disease
CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
CC protein
XX

[illegible]

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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148694P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.

PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 64.0%; Score 483.5; DB 3; Length 147;
Best Local Similarity 65.0%; Pred. No. 1.2e-47;
Matches 93; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVGAKGLENTDYLCNNDPYPAILKCRSQEQKSSATGKGTTPWNNFIPTV 60
DB 1 MPHGTLEVLVLSAKGLEADADFLNNMDPYVOLTCRTQDQKSNVAEGNGTTPWNETFIPTV 60
QY 61 SDRTTDLVIKLMDSDTGTAADDFVGEATIPLEAVYTERSIPTLYNVVKGEKCYGKEIKVGL 120
DB 61 SEGTTELKAKIFDKDVGTEDDAVGEATIPLEPVFVEGSIPTTAYNVVKKDEEYKGEIWWAL 120
QY 121 TFTPEDTRORGLPED-FGGWKOS 142
DB 121 SFKPSGNRSRGMDEERSYGGWKNS 143

RESULT 9
AAB44510
ID AAB44510 standard; protein; 202 AA.
XX
AC AAB44510;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 34.
XX
KW Plant viral movement protein; transport; transgenic plant;
XX
OS Zea mays.
XX
PN WO200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
DR N-PSDB; AAC79364.
XX
PS Claim 23; Page 52; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 202 AA;
Query Match 62.2%; Score 470.5; DB 3; Length 202;
Best Local Similarity 72.2%; Pred No. 5.8e-46;
Matches 91; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 1 MVHGTLEVLVGAAGLENTDYLCNMDPYAILKCRSQKSSIAATGKTTPWNNENFIPTV 60
Db 76 MAQGTLEVLVGAAGLENTDYLSNMDPYALLQCRSHEQKSSVASKGCEPEWNETFPTV 135

OY 61 SDRITDLVILKMSDTCGADDFVGEATIPLEA-VYTERSIPPTLYNVVKGKYGKGEIKVG 119
Db 136 SNGAXELFIKLDSDGGDDDFVGEATIPLEASLHGKFAFLPTVYNVVKGDEYRGEIKVG 195

OY 120 LTFTPE 125
Db 196 LTFTPE 201

RESULT 10
AAB44494
ID AAB44494 standard; protein; 130 AA.
XX
AC AAB44494;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 2.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Vitis sp.
XX
PN WO200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
WPI; 2000-638467/61.
DR N-PSDB; AAC79348.
XX
Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 34-35; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

```
XX SQ Sequence 130 AA;
Query Match 60.7%; Score 459; DB 3; Length 130;
Best Local Similarity 65.9%; Pred No. 6.9e-45;
Matches 8; Conservative 23; Mismatches 16; Indels 6; Gaps 2;

OY 1 MVHGTLEVLVGAAGLENTDYLCNMDPYAILKCRSQKSSIAATGKTTPWNNENFIPTV 60
Db 1 MPQGTLEVLVSAKLENTDFLCNMDPYVVLTCRTQKSSVASKGSDPEWNEHFVTI 60

OY 61 SDRITDLVILKMSDTCGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKYGKGEIKVG 119
Db 61 SEGISELTIKMDSGSGDDFVGEATIPLEALFTGSLPSTGCTMLLTKTKEYGKGEIKVG 120

OY 120 LTFTPEDTRORG 131
Db 121 LTFT-----QKG 127

RESULT 11
AAB44507
ID AAB44507 standard; protein; 145 AA.
XX
AC AAB44507;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 28.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Oryza sativa.
XX
PN WO200060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
WPI; 2000-638467/61.
DR N-PSDB; AAC79361.
XX
Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 49; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
```

XX SQ Sequence 145 AA;
Query Match 60.1%; Score 454.5; DB 3; Length 145;
Best Local Similarity 65.2%; Pred. No. 2.7e-44;
Matches 90; Conservative 16; Mismatches 31; Indels 1; Gaps 1;
QY 1 MVHGTLVLVGAAGKLENTDYLGNMPPYAILKCRSQEOKSSSIATGKTTPEWNEPIFTV 60
DB 1 MVHGKLEVLVCAKGLDITDFLNMDPPYVILTCRTQEQKSSVAKGAGSPENWNETVFTV 60
QY 61 SDRTDLVILKMSDITGTDADFVGEATIPLEAVYITERSIPTLYNVVKGKCYGKIKVGL 120
DB 61 SDDVPQLNVKIMSDAFSADDFVGEANIPLPEVFLGSLPPAHRVVVKEEKYCGEIKVAL 120
QY 121 TFTP-EDTRQGLPDEFG 137
DB 121 TFTPAAETRRHHNENEG 138

RESULT 12
AAB44497
ID AAB44497 standard; protein; 140 AA.
XX AC AAB44497;
XX DT 06-FEB-2001 (first entry)
XX DE Plant viral movement protein SEQ ID 8.
XX DE Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX OS Hevea brasiliensis.
XX PN WO200060088-A2.
XX PD 12-OCT-2000.
XX PF 06-APR-2000; 2000WO-US0009110.
XX PR 07-APR-1999; 99US-0128092P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Krebbers E, Weng Z, Cahoon RE;
XX WP1; 2000-638467/61.
XX DR N-PSDB; AAC79351.
XX PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX PS Claim 10; Page 38; 62pp; English.

XX CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilise
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance

XX SQ Sequence 140 AA;
Query Match 58.9%; Score 445; DB 3; Length 140;
Best Local Similarity 68.0%; Pred. No. 3.2e-43;
Matches 83; Conservative 17; Mismatches 22; Indels 0; Gaps 0;
QY 4 GTLEVLVCAKGLNTDYLGNMPPYAILKCRSQEOKSSSIATGKTTPEWNEPIFTVSDR 63
DB 4 GTFEVLVCAKGLNTDFLNGVDPYVVLACRTQEQKSSVASGSGEPENKEFSEVSDG 63
QY 64 TTDLVILKMSDITGTDADFVGEATIPLEAVYITERSIPTLYNVVKGKCYGKIKVGLTPT 123
DB 64 DTLELTLMKIMSDVGAADDFVGEATIPLEPLFLEGNLPSYAYKVVKEQYKGEITVGLTPT 123
QY 124 PE 125
DB 124 PE 125
RESULT 13
AAB44509
ID AAB44509 standard; protein; 142 AA.
XX AC AAB44509;
XX DT 06-FEB-2001 (first entry)
XX DE Plant viral movement protein SEQ ID 32.
XX DE Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX OS Triticum aestivum.
XX PN WO200060088-A2.
XX PD 12-OCT-2000.
XX PF 06-APR-2000; 2000WO-US0009110.
XX PR 07-APR-1999; 99US-0128092P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Krebbers E, Weng Z, Cahoon RE;
XX WP1; 2000-638467/61.
XX DR N-PSDB; AAC79363.
XX PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX PS Claim 10; Page 51; 62pp; English.

XX CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilise
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance


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PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149829P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 05-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.5%; Score 419.5; DB 3; Length 133;
Best Local Similarity 58.7%; Pred. No. 2.8e-40;
Matches 84; Conservative 15; Mismatches 29; Indels 15; Gaps 2;

QY 1 MVHGTLEVLVCAKGLNTDYLCNMDPYAILKCRSQEQKSSIATGKTTPENENFIPTV 60
Db 1 MPHGTLEVLVSAKGLNEDADPL-----NOKSNVAEGMGTTPENNETFIPTV 46
QY 61 SDRTTDLVIKLMDSDTGTADDFVGRATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVCL 120
Db 47 SEGTTTELKAKIPDKVGTEDDVGATIPLEPVFVSGSIPPTAYNVVVDKDEYKGEIWWAL 106
QY 121 TFTPEDTRQRLPED-FGGWKOS 142
Db 107 SFPKPSNRSGMDEESYGGWKNS 129

RESULT 15
AAB44508
ID AAB44508 standard; protein; 149 AA.
XX
AC AAB44508;
XX
DT 06-FEB-2001 (first entry)
XX
DE Plant viral movement protein SEQ ID 30.
XX
KW Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression.
XX
OS Glycine max.
XX
PN WO2000060088-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009110.
XX
PR 07-APR-1999; 99US-0128092P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Krebbers E, Weng Z, Cahoon RE;
XX
DR WPI; 2000-638467/61.
XX
N-PSDB; AAC79362.
XX
PT Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
PS Claim 10; Page 50-51; 62pp; English.
XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC Proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
```

CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 149 AA;

Query Match 53.5%; Score 404.5; DB 3; Length 149;
Best Local Similarity 52.1%; Pred. No. 1.8e-38;
Matches 76; Conservative 29; Mismatches 38; Indels 3; Gaps 1;
Qy 1 MVHGTLEVLVYKAGLENTDYLGNMDPYAILKCRSQEQKSSIAATGKGTTPWNNENFIFTV 60
Db 1 MPRGTLEVLVISAKGIDNDLSSIDPVIITYRAQEKSTVQEDAGSKPQWNSFLFTV 60
Qy 61 SDRTDLVILKMDSDTGTADDFVGEATIPLEAVYTERSIPETLYNVVKGEYKCGEIKVGL 120
Db 61 SDSASELNLIKMDKNFSDQDCLGEATIHLDVPFAGSIPETAYKVKWDEEYCGEIKVAL 120
Qy 121 TFTPEDTQRGL---PEDFGGWKQSS 143
Db 121 TFTAERNEEQYDAPEESYGGWKSS 146

Search completed: January 6, 2005, 13:59:22
Job time : 156 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 13:48:09 ; Search time 41 Seconds
(without alignments)
335.585 Million cell updates/sec

Title: US-09-913-569B-6
Perfect score: 756
Sequence: 1 MVHGTLEVLVVGAKGLEN...PEDTRQRLPEDFGWKQSS 143

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605.5	80.1	144	2 T50649	elicitor-responsiv
2	486.5	64.4	147	2 H96657	probable elicitor-
3	455.5	60.3	143	2 T04091	hypothetical prote
4	259	34.3	156	2 T04363	FIERG2 protein - r
5	246.5	32.6	159	2 T04314	elicitor responsiv
6	240.5	31.8	156	2 T47686	phloem protein [im
7	177	23.4	150	2 T50648	FI5K9.2 protein -
8	149.5	19.8	1020	2 E86155	hypothetical prote
9	145	19.2	279	2 T05421	CLB1-like protein
10	129.5	17.1	574	2 T51799	probable membrane
11	123.5	16.3	1186	2 S61647	protein T1N15.21
12	120	15.9	505	2 T04143	hypothetical prote
13	119	15.7	200	2 E96525	protein T1N15.21
14	118.5	15.7	804	2 T25673	hypothetical prote
15	117.5	15.5	887	2 S70642	ubiquitin ligase N
16	117	15.5	168	2 F96762	hypothetical prote
17	115	15.2	591	2 S54788	calcium-stimulated
18	114	15.1	369	2 T04947	hypothetical prote
19	112.5	14.9	675	2 T01234	probable anthranil
20	112.5	14.9	795	2 T47964	hypothetical prote
21	112	14.8	400	2 JC2473	doc2 protein - hum
22	111.5	14.7	334	2 A85067	hypothetical prote
23	111.5	14.7	468	2 F71422	hypothetical prote
24	111	14.7	180	2 A84426	hypothetical prote
25	111	14.7	524	2 G94595	hypothetical prote
26	109	14.4	174	2 F96732	hypothetical prote
27	108	14.3	832	2 H84848	phospholipase D [i
28	107	14.2	737	2 H96538	hypothetical prote
29	106.5	14.1	972	2 T47922	anthranilate phosph

30 105.5 14.0 1735 2 A57607 Munc13-1 - rat
31 104.5 13.8 751 1 T29357 1-phosphatidylinos
32 104 13.8 510 2 T50526 CalB protein - Ara
33 104 13.8 514 2 T41648 C2 domain family p
34 104 13.8 1429 2 T41699 C2-domain family p
35 104 13.8 1430 2 T12449 hypothetical prote
36 103.5 13.7 2207 2 T42759 Munc13-3 protein -
37 102.5 13.6 672 1 KIHUCA protein kinase C (
38 102.5 13.6 672 1 KIMSCA protein kinase C (
39 102.5 13.6 672 1 KIRBC protein kinase C (
40 102.5 13.6 672 1 KIRTC protein kinase C (
41 102 13.5 441 2 A40707 synaptotagmin - Ca
42 101.5 13.4 604 2 T49307 hypothetical prote
43 101.5 13.4 773 2 T46010 anthranilate phosph
44 101.5 13.4 820 2 T46412 ubiquitin-protein
45 101 13.4 290 2 T07080 shock protein SRC2

ALIGNMENTS

RESULT 1

T50849

elicitor-responsiv gene 3 [imported] - rice

C;Species: Oryza sativa (rice)

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C;Accession: T50649

R;Kim, C.Y.; Cheon, S.Y.; Cho, M.J.

Submitted to the EMBL Data Library, September 1998

A;Description: Identification and Characterization of Fungal Elicitor Responsive Rice C

A;Reference number: 225156

A;Accession: T50649

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-144 <KIM>

A;Cross-references: UNIPROT:O82550; EMBL:AF090698; PIDN:AAC35866.1

C;Genetics:

A;Gene: ERG3

Query Match 80.1%; Score 605.5; DB 2; Length 144;
Best Local Similarity 79.9%; Pred. No. 3.5e-51;
Matches 115; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MVHGTLEVLVVGAKGLEN...PEDFGWKQSS 143
Db 1 MVHGTLEVLVVGAKGLEN...PEDFGWKQSS 144
Qy 61 SDRTDLVIKLMDS...PLEAVYTERSIPTLYNNVKGKCEIKVGL 120
Db 61 THNATELIIKLMDS...PLEAVYTERSIPTLYNNVKGKCEIKVGL 120
Qy 121 TFTPEDTRQRL...PEDFGWKQSS 143
Db 121 TFTPEDTRQRL...PEDFGWKQSS 144

RESULT 2

H96657

probable elicitor-responsiv gene F9N12.16 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: H96657

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A;Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H96857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <STO>
C;Cross-references: UNIPROT:Q9C8S6; GB:AB005173; NID:g6997198; PIDN:AAF34860.1; GSPDB:GN
A;Gene: F9N12.16
A;Map position: 1

Query Match 64.4%; Score 486.5; DB 2; Length 147;
Best Local Similarity 65.0%; Pred. No. 1.1e-39;
Matches 93; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

QY 1 MVHGTELVLLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSIAATGKTTPWNNENFIPTV 60
Db 1 MPHGTELVLLVSAKGLDADFLNNMDPYVQLTCTQKSNVAGGTTPEWNETIFIV 60

QY 61 SDRITDVLKIMDSDTGTDADDFVGEATIPLEAVYTERSIPPTLYNVVKGKYGKIKVGL 120
Db 61 SEGTTLAKAKIFDKDVGTEDDAVGEATIPLEPVFVSGSIPPTAYNVVKKDEYKGEIIVAL 120

QY 121 TFTPEDTRQGLPED-FGGWKQS 142
Db 121 SFRPSNRSRGMDSESYGGWKNS 143

RESULT 3
T04091
hypothetical protein - maize
C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04091
R;Betawar, N.M.; Baysdorfer, C.
submitted to the EMBL Data Library, July 1996
A;Description: Novel maize gene.
A;Reference number: Z15202
A;Accession: T04091
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-143 <BET>
A;Cross-references: UNIPROT:Q24582; EMBL:U64437; NID:g1498054; PIDN:AAB06331.1; PID:g149
A;Experimental source: strain B73

Query Match 60.3%; Score 455.5; DB 2; Length 143;
Best Local Similarity 62.1%; Pred. No. 1e-36;
Matches 90; Conservative 18; Mismatches 28; Indels 9; Gaps 3;

QY 1 MVHGTELVLLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSIAATGKTTPWNNENFIPTV 60
Db 1 MVHGTELVLLVSAKGLDADFLNNMDPYVQLTCTQKSNVAGGTTPEWNETIFIV 60

QY 61 SDRITDVLKIMDSDTGTDADDFVGEATIPLEAVYTERSIPPTLYNVVKGKYGKIKVGL 120
Db 61 SDTTPQLHLKIMDSDL-TNDDFVGERTIPLEAVFQSGSLPPAVHPVVKEEKYCGEVKAL 119

QY 121 TFTPEDTRQGLPED-----FGW 139
Db 120 TTFPAATRR--PDDNEEGPPYSSW 142

RESULT 4
T04363
FIERG2 protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04363
R;Kim, C.Y.; Choe, M.S.; Jeong, S.Y.; Bae, C.G.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
A;Description: Isolation and characterization of early rice genes by a fungal elicitor
A;Reference number: Z15277
A;Accession: T04363
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-156 <KIM>
A;Cross-references: UNIPROT:O50006; EMBL:U95136; NID:g2920838; PIDN:AAC04628.1; PID:g29.
C;Genetics:
A;Gene: FIERG2

Query Match 34.3%; Score 259; DB 2; Length 156;
Best Local Similarity 41.3%; Pred. No. 1e-17;
Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;

QY 4 GTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSIAATGKTTPWNNENFIPTVSDR 63
Db 5 GVLEVHLVDKAGLTGNDFLGKIDPVVQYRSQERKSSVARQDGKNPSNNEVFKFQI 64

QY 64 TT-----DLVIKIMDSDTGTDADDFVGEAT-----IPLEAVYTERSIPPTLYNVVKGK-Y 112
Db 65 AATGQHLFLRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWMSSESKHRVVLADKY 124

QY 113 CGEIKVGLTFTPTEDTRQGLPEDFGWKQS 142
Db 125 HGEIRVSLTFT-ASAKADHAEQVGVWAHS 153

RESULT 5
T04314
FIERG1 protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04314
R;Kim, C.Y.; Choe, M.S.; Jeong, S.Y.; Bae, C.G.; Cheong, Y.H.; Han, C.D.; Cho, M.J.
submitted to the EMBL Data Library, March 1997
A;Description: Isolation and characterization of early rice genes by a fungal elicitor
A;Reference number: Z15277
A;Accession: T04314
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-159 <KIM>
A;Cross-references: UNIPROT:O50005; EMBL:U95135; NID:g2920836; PIDN:AAC04627.1; PID:g29.
C;Genetics:
A;Gene: FIERG1
A;Note: fungal inducible gene

Query Match 32.6%; Score 246.5; DB 2; Length 159;
Best Local Similarity 40.5%; Pred. No. 1.6e-16;
Matches 62; Conservative 22; Mismatches 54; Indels 15; Gaps 5;

QY 4 GTLEVLVGAAGLENTDYL---CNMDPYAILKCRSQEQKSSIAATGKTTPWNNENFIPTV 60
Db 5 GVLEVHLVDKAGLTGNDFLGKIDPVVQYRSQERKSSVARQDGKNPSNNEVFKFQI 64

QY 61 SDRIT-----DLVIKIMDSDTGTDADDFVGEAT-----IPLEAVYTERSIPPTLYNVVKGK 110
Db 65 NSTAATGQHKLFRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWMSSESKHRVVLAD 124

QY 111 K-YCGEIKVGLTFTPTEDTRQGLPEDFGWKQS 142
Db 125 KTYHGEIRVSLTFT-ASAKADHAEQVGVWAHS 156

RESULT 6
T047686
elicitor responsive/phloem-like protein - Arabidopsis thaliana
N;Alternate names: protein T22E16.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T047686
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lencke, K.; Mayer, K.I.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24472
A;Accession: T047686
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <BEN>
A;Cross-references: UNIPROT:Q9M2T2; EMBL:AL132975

A:Experimental source: cultivar Columbia; BAC clone T22E16
C:Genetics:
A:Map position: 3
A:Introns: 23/1; 45/1; 92/2; 137/3
A:Note: T22E16.130

Query Match 31.8%; Score 240.5; DB 2; Length 156;
Best Local Similarity 35.5%; Pred. No. 6.1e-16;
Matches 55; Conservative 33; Mismatches 52; Indels 15; Gaps 6;

Qy 1 MVHCTLEVLVAGKLENTDYLNCMDPYAILKCRSQEQKSSIA-TGKGTTPWNNF--- 56
Db 1 MAVGILEVLSISGGLKRLKIDPVVEIQYQGRKSSVAKEDGGRNPTWMDKLWR 60
Qy 57 -IFTVSDRTTDLVIKLMDSDTGTADDVFGEATIPLEAVYT-----ERSIPPTLYNVVKG 109
Db 61 AEPFGSGADYKLIYKVMHDHFTSSDDFIGEATVHVKELLENGVEKGTAELRPTKYNIVDS 120

Qy 110 E-KYCGEIKVGLTTPEDTRQGLP-EDFGWKOS 142
Db 121 DLSFVGBELLIGVSYSL--LQDRGMDGQFGGWKHS 153

RESULT 7
T50648
phloem protein [imported] - winter squash
C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50648

R:Xoconostle-Cazares, B.; Xiang, Y.; Ruiz-Medrano, R.; Wang, H.L.; Monzer, J.; Yoo, B.C.
Science 283, 94-98, 1999
A:Title: Plant paralog to viral movement protein that potentiates transport of mRNA into
A:Reference number: 225155; MUID:99102700; PMID:9872750

A:Accession: T50648
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-150 <XOC>
A:Cross-references: UNIPROT:Q92T47; EMBL:AF079170; PIDN:AAD05496.1
A:Experimental source: cultivar Big max
C:Genetics:
A:Gene: PP16

Query Match 23.4%; Score 177; DB 2; Length 150;
Best Local Similarity 32.8%; Pred. No. 7.7e-10;
Matches 43; Conservative 27; Mismatches 49; Indels 12; Gaps 4;

Qy 4 GTLEVLVAGKLENTDYLCH-MDPYAILKCRSQEQKSSATGKGTTPWNNFIFTV-- 60
Db 4 GMMEVHLISGKGLQAHPLNKPIDPYAEINFKGQGRMSKVNAGPNPLWDEKFKFLAEY 63
Qy 61 --SDRTTDLVIKLMDSDTGTADDVFGEATIPLEAVYTE-----RSIPPTLYNVVKG-K 111
Db 64 PGSGGDPHILFKVMHDHDAIDGDDYIGVDKIDVKLLAEGVRKKGKSEMPRMHYVLAHKIH 123

Qy 112 YCGEIKVGLTF 122
Db 124 FKGEIVGVSF 134

RESULT 8
E86165
P15K9.2 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86165
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86165
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1020 <STO>
A:Cross-references: UNIPROT:Q9ZVT9; GB:A8005172; NID:g3850588; PIDN:AAC72128.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 19.8%; Score 149.5; DB 2; Length 1020;
Best Local Similarity 30.5%; Pred. No. 3.8e-06;
Matches 39; Conservative 27; Mismatches 55; Indels 7; Gaps 4;

Qy 6 LEVLLVCAKLENTDYLNCMDPYAILKCRSQEQKSSATGKGTTPWNNFIFTVSDRTT 65
Db 3 LQVRVVEARNLPAMDNLGFSDPVRLQLGKQRSTKVK-KNLNPKWTEDEFSFGVDDLND 61
Qy 66 DLVIKLMDSDTGTADDVFGEATIPLEAVY--TERSIPPTLYNV---VKG-EKYCGEIKVG 119
Db 62 ELVSVVLDEKYNDDFVGQVRVSVSLVFDENQSLGTVMYPLNPKKSKKDCGEILLK 121

Qy 120 LTFPTPDT 127
Db 122 ICFSQKNS 129

RESULT 9
T05421
hypothetical protein F28A23.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05421
R:Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.;
submitted to the Protein Sequence Database, October 1998

A:Reference number: Z15415
A:Accession: T05421
A:Molecule type: DNA
A:Residues: 1-279 <BEV>
A:Cross-references: UNIPROT:O49490; EMBL:AL021961
A:Experimental source: cultivar Columbia; BAC clone F28A23
C:Genetics:
A:Map position: 4
A:Introns: 38/1; 73/1; 115/2; 139/2; 151/3
A:Note: F28A23.90

Query Match 19.2%; Score 145; DB 2; Length 279;
Best Local Similarity 32.6%; Pred. No. 2e-06;
Matches 28; Conservative 22; Mismatches 36; Indels 0; Gaps 0;

Qy 11 VGAKLENTDYLNCMDPYAILKCRSQEQKSSATGKGTTPWNNFIFTVSDRTTDLVIK 70
Db 39 VGCQKLDTEFWFRQDPYVVLVEYGGRSRTRTCTDGGKNVAFQEKFIITLIEGLRDLKVA 98
Qy 71 LMSDSTGTADDVFGEATIPLEAVYTE 96
Db 99 VWSNTLSTDDDFIGNATIQLQKVLQ 124

RESULT 10
T51799
CLB1-like protein - Arabidopsis thaliana
N:Alternate names: protein T5K6_90
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51799
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voickaert, G.; E;
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25455
A:Accession: T51799
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-574 <BEV>
A;Cross-references: UNIPROT:O9FY55; EMBL:AL391222
A;Experimental source: cultivar Columbia; BAC clone T5K6
C;Genetics:
A;Map position: 5
A;Introns: 35/3; 77/3; 94/3; 135/1; 177/3; 211/3; 236/3; 263/2; 313/3; 390/3
A;Note: T5K6_90

Query Match 17.1%; Score 129.5; DB 2; Length 574;
Best Local Similarity 28.5%; Pred. No. 0.00016;
Matches 39; Conservative 21; Mismatches 50; Indels 27; Gaps 6;
QY 4 GTLEVLVGAAGLENTDYLGNMPPYAILKCR--SQEQKSSIAATGKTTPWENEFITVVS 61
DB 271 GKLDVKVQAQKLANCKMIGKSDPYAIVFIRPLPDRTKTKTKTSLSLNPIWNEHEFEFIVE 330
QY 62 DRTTDLVVKLMSDGTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGEEK-VG 119
DB 331 DVSTQHLTVRVFDEGVGSQLIGNAQVPLNEL-----VP-----GKVKDIW 372
QY 120 LTFPE-----DTRQRG 131
DB 373 LKLVKLEIQDITNRC 389

RESULT 11
S61647
Probable membrane protein YOR086c - Yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O3141; hypothetical protein YOR3141c
C;Species: Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
R;Accession: S61647; S66971
R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia submitted to the EMBL Data Library, December 1995
A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A;Reference number: S61643
A;Accession: S61647
A;Molecule type: DNA
A;Residues: 1-1186 <BEN>
A;Cross-references: UNIPROT:Q12466; EMBL:X94335; NID:g1262139; PID:e217724; PID:g1164933
R;Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoerge, W. submitted to the Protein Sequence Database, July 1996
A;Reference number: S66965
A;Accession: S66971
A;Molecule type: DNA
A;Residues: 1-1186 <VOS>
A;Cross-references: EMBL:Z74994; NID:g1420251; PID:e251995; PID:g1420252; MIPS:YOR086c
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005612
A;Map position: 15R
C;Keywords: transmembrane protein
F;105-125/Domain: transmembrane #status predicted <TM1>
F;129-145/Domain: transmembrane #status predicted <TM2>
F;175-231/Domain: transmembrane #status predicted <TM3>

Query Match 16.3%; Score 123.5; DB 2; Length 1186;
Best Local Similarity 28.7%; Pred. No. 0.0015;
Matches 39; Conservative 26; Mismatches 52; Indels 19; Gaps 6;
QY 4 GTLEVLVGAAGLENTDYLGNMPPYAILKCRSQEQ--KSSIAATGKTTPWENEFITV 60
DB 992 GDLTMSRSANLITASDLNGSYDPLKYVINNEEDCAKTKVKV-KTLNPKWDEGTIQI 1050
QY 61 SDRTTDLV-IKLMDSDTGADDFVGEATIPLEAV-----YTERSIPPTLYNVVKGKCYGEE 115
DB 1051 NNRLNDVLRIKVMWDWTSADDTTGTAEIPLNKVKVETGTELDVP-----VEGLENAQ 1104
QY 116 ----IKVGLTTPEDT 127
DB 1105 DGGMLHLAFSPKPRYT 1120

RESULT 12

T04143
CLB1 protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04143
R;Kiyosue, T.; Ryan, C.A.
Plant Mol. Biol. 35, 969-972, 1997
A;Title: A novel gene of tomato preferentially expressed in fruit encodes a protein with
A;Reference number: 215238; MUID:98088022; PMID:9426616
A;Accession: T04143
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-505 <KI>
A;Cross-references: UNIPROT:O48645; EMBL:AB001389; NID:g2789433; PID:BAA24382.1; PID:g2789433

Query Match 15.9%; Score 120; DB 2; Length 505;
Best Local Similarity 26.8%; Pred. No. 0.0011;
Matches 34; Conservative 22; Mismatches 63; Indels 8; Gaps 2;
QY 4 GTLEVLVGAAGLENTDYLGNMPPYAILKCRSQEQKSSIAATGKTTPWENEFITVSDR 63
DB 262 GKLTVTIVKANGLNHEMIGKSDPYAVVHIRPLEFKVTKTKTIDNNLNPNVMDQTFELJAE DK 321
QY 64 -TTDLVVKLMSDGTGADDFVGEATIPLEAVYTE-----RSIPPTLYNVVKGKCYGEE 115
DB 322 ETQSLFIEVFDKDNIGQDRMGVAKLPUNELVADAKEIELRLLPKLDMLKVKDKDGRGT 381
QY 116 IKVGLTF 122
DB 382 ITIKVLY 388

RESULT 13

E96525
protein T1N15.21 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Accession: E96525
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <STO>
A;Cross-references: UNIPROT:Q9LP65; GB:AE005173; NID:g8778695; PID:AAF9703.1; GSPDB:G
C;Genetics:
A;Gene: T1N15.21
A;Map position: 1

Query Match 15.7%; Score 119; DB 2; Length 200;
Best Local Similarity 24.2%; Pred. No. 0.00043;
Matches 40; Conservative 26; Mismatches 57; Indels 42; Gaps 6;
QY 4 GTLEVLVGAAGLENTDYLGNMPPYAILKCRSQEQKSSIAATGKTTPWENEFITVSDR 63
DB 42 GLLRIRKRGVNLAVRD-LNSSDPYVVVQAKQKLRVIY-KNVNPNEDDLTSLVSDP 99
QY 64 TTDLVVKLMSDGTGADDFVGEA-----TIPLEAVYTERSIPPTLYNVV 107
DB 100 NLTVLTVVDYDTFTTKDKMGDAEFGIKPFVNALKMHLHDLPSGTIVT--TVQPSRDNCL 157
QY 108 KGEK-----YCGEIKVGLTFPTPEDTRQRL 132


```

Qy 59 TVSDRTDLVIKLMDSGTGTAADFVGEATIPLEAVYTER----SPDPTLYNVV-----KGE 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 RVLPPQQRHILFEVDENRLTRDDELFGQVDVPLPLPTENPRMERPYTFKDFVLHPRSHKS 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 111 KYCGEIKVGLTFTPED 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 195 RVKGYLRKMTYLPKN 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: January 6, 2005, 14:03:30
Job time : 43 secs

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Db 158 ABEESRVWSDGKLVQDIVLRHVRHVECEVAQLQWI--DLPGKGL 200

RESULT 14

T25673

hypothetical protein D2092.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T25673

R:Gattung, S.; Maggi, L.

submitted to the EMBL Data Library, February 1997

A:Description: The sequence of C. elegans cosmid D2092.

A:Reference number: Z20067

A:Accession: T25673

A:Status: preliminary; translated from CB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-804 <CAT>

A:Cross-references: UNIPROT:P91199; EMBL:U88167; PIDN:AAB42222.1; GSPDB:GN00019; CBSP:D2092

A:Experimental source: strain Bristol N2; clone D2092

C:Genetics:

A:Gene: CBSP:D2092.1

A:Map position: 1

A:Introns: 34/3; 76/1; 150/2; 206/1; 218/1; 301/2; 451/1; 498/2; 589/3; 631/3; 686/3; 79/3

Query Match 15.7%; Score 118.5; DB 2; Length 804;

Best Local Similarity 26.4%; Pred. No. 0.0027;

Matches 38; Conservative 28; Mismatches 57; Indels 21; Gaps 6;

QY 9 LLVGAKGLENTDYLCNMDPVAILK-CRSEQKSSIAATGKTTPWNNENIFTVSDRTTDL 67

DB 450 LVFGAEDLVAKDFGGKSDPFVLELVNTRVQNTIY--KTLSPSWNKIYTFVAVKDIHTCL 507

QY 68 VIKLMDSDGTGTDADFGEATIPLEAVYTERSIPPTLVN-----VKGEKYC----- 113

DB 508 QVTIYDEDPNNRPEFLGRVQIPLKSI---RNCQKRWYGLKDEKLKRVRKGEVLELMDVIW 564

QY 114 GEIKVGL-TFTPEDTQRGLPEDF 136

DB 565 NPIRAAIIRTKPKKEIKYMSQEQKP 588

RESULT 15

S70642

ubiquitin ligase Nedd4 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S70642

R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

EMBO J. 15, 2371-2380, 1996

A:Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+)

A:Reference number: S70642; MUID:96221297; PMID:8665844

A:Accession: S70642

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-887 <STA>

A:Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:gl2933646; PIDN:AAB48949.1; PTD:gl2933646

C:Genetics:

A:Gene: Nedd4

C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquitin ligase Nedd4 - rat (fragment)

F:54-167/Domain: protein kinase C C2 region homology <KC2>

F:246-283/Domain: WW repeat homology <WW1>

F:402-439/Domain: WW repeat homology <WW2>

F:459-496/Domain: WW repeat homology <WW3>

F:555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 15.5%; Score 117.5; DB 2; Length 887;

Best Local Similarity 24.3%; Pred. No. 0.0039;

Matches 33; Conservative 28; Mismatches 58; Indels 17; Gaps 4;

QY 6 LEVLLVGAKLENTDYLCNMDPVAILKCRSEQKSSIAATG-----KGTTPWNNENFTF 58

DB 77 VRVKVITAGTIGLAKKDIILGASDPY--VRVTLYDPMGSLTTSVQTKTKKSLNPKWNEILF 134

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2005, 13:49:13 ; Search time 41 Seconds
(without alignments)
231.304 Million cell updates/sec

Title: US-09-913-569B-6
Perfect score: 756
Sequence: 1 MVHGTLEVLVGAKGLENTD.....PEDTRQRLPEDFGMKQSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pdp.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*

5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pdp.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122.5	16.2	927	3	US-08-895-601-6
2	113	14.9	1026	4	US-09-248-796A-16128
3	112.5	14.9	291	4	US-09-248-796A-15333
4	106	14.0	988	4	US-09-382-552-233
5	106	14.0	2080	4	US-09-382-552-2
6	104.5	13.8	82	4	US-09-382-552-88
7	104.5	13.8	799	3	US-08-909-954-4
8	102.5	13.6	672	4	US-10-092-138A-27
9	102.5	13.6	672	4	US-09-538-092-943
10	99.5	13.2	233	4	US-09-248-796A-18185
11	97.5	12.9	916	4	US-09-417-157-73
12	96.5	12.8	172	4	US-09-270-767-43037
13	96.5	12.8	766	3	US-08-539-205A-4
14	96.5	12.8	766	4	US-09-392-163A-4
15	96	12.7	673	4	US-09-538-092-853
16	95	12.6	623	4	US-09-270-767-45228
17	94.5	12.5	324	4	US-09-270-767-44986
18	92	12.2	744	3	US-08-738-884-5
19	92	12.2	744	4	US-10-096-961A-5
20	89.5	11.8	916	4	US-09-688-078-9
21	88.5	11.7	804	3	US-08-909-954-2
22	86.5	11.4	372	4	US-09-107-532A-6792
23	86.5	11.4	1154	4	US-09-688-078-7
24	86	11.4	132	4	US-09-270-767-45401
25	85	11.2	139	4	US-09-294-298A-17
26	85	11.2	744	3	US-09-738-884-4
27	85	11.2	744	4	US-10-096-961A-4

28	84.5	11.2	1001	4	US-09-688-078-2	Sequence 2, Appli
29	84	11.1	140	2	US-08-609-049A-16	Sequence 16, Appl
30	84	11.1	140	3	US-09-170-996-16	Sequence 16, Appl
31	84	11.1	641	3	US-09-422-869-26	Sequence 26, Appl
32	83.5	11.0	639	3	US-09-422-869-25	Sequence 25, Appl
33	83.5	11.0	640	4	US-09-308-345A-7	Sequence 7, Appli
34	83	11.0	336	4	US-09-270-767-33924	Sequence 33924, A
35	83	11.0	336	4	US-09-270-767-49141	Sequence 49141, A
36	83	11.0	671	6	5266464-2	Patent No. 5266464
37	81.5	10.8	640	4	US-09-308-345A-2	Sequence 2, Appli
38	77	10.2	1590	4	US-09-617-099B-1	Sequence 1, Appli
39	76.5	10.1	183	4	US-09-583-110-4832	Sequence 4832, Ap
40	76.5	10.1	205	4	US-09-270-767-42337	Sequence 42337, A
41	75.5	10.0	115	3	US-09-036-315-8	Sequence 8, Appli
42	75.5	10.0	422	3	US-08-872-979-8	Sequence 8, Appli
43	75	9.9	117	3	US-09-036-315-6	Sequence 6, Appli
44	75	9.9	812	1	US-08-446-794A-2	Sequence 2, Appli
45	75	9.9	812	1	US-08-750-007-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-895-601-6
; Sequence 6, Application US/08895601
; Patent No. 6060262
; GENERAL INFORMATION:
; APPLICANT: Beer-Romero, Peggy
; APPLICANT: Strack, Peter J.
; APPLICANT: Glass, Susan J.
; APPLICANT: Rolfe, Mark
; TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,
; TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,601
; FILING DATE: 16-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-096.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-895-601-6

Query Match 16.2% Score 122.5; DB 3; Length 927;
Best Local Similarity 25.1%; Pred. No. 7.1e-06;
Matches 42; Conservative 25; Mismatches 69; Indels 31; Gaps 6;
Qy 2 VHGTLE-----VLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSIATG----- 45
Db 35 VFGLEDENSRIVRVRIAGIGLAKKIDILGASDPY--VVRTLYDPMNGVLTSVQTKIK 92

Matches	35;	Conservative	22;	Mismatches	63;	Indels	9;	Gaps	3
Qy	4	GTLEVLVAGAGLENTDYL	CNMDPYAILKCRSQKSS	IATGKGTTP	EWNNFIFTVS	-D	62		
Db	55	GTLLVMVIRAKHLPNR	RKLKDKQSPYVVARIGT	VAKTAAAFRAQGT	PEWHEMRFELSRE	114			
Qy	63	RTTDLVLKLMDSDTG	TADDFVGEATIPLEAVY	TE-----RS	IPPTLYNVVKG	KYCGE	115		
Db	115	RKPLKIDVLID-ET	KNDPTPIGNVEIDAS	IIFTNPENNENK	YIKWYDLTLN	RRAGM	173		
Qy	116	IKVGLTFTP	124						
Db	174	IYLEMTFYP	182						

RESULT 4
 US-09-382-552-233
 ; Sequence 233, Application US/09382552
 ; Patent No. 6673909
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Jr., Robert H.
 ; APPLICANT: Liu, Jing
 ; APPLICANT: Aoki, Masashi
 ; APPLICANT: Ho, Meng
 ; APPLICANT: Matsuda-Asada, Chie
 ; TITLE OF INVENTION: DYSPERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
 ; TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
 ; FILE REFERENCE: 00786/399002
 ; CURRENT APPLICATION NUMBER: US/09/382,552
 ; CURRENT FILING DATE: 1999-08-25
 ; EARLIER APPLICATION NUMBER: US 60/097,927
 ; EARLIER FILING DATE: 1998-08-25
 ; NUMBER OF SEQ ID NOS: 233
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 233
 ; LENGTH: 988
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-382-552-233

Query Match	14.0%;	Score	106;	DB	4;	Length	988;
Best Local Similarity	27.9%;	Pred. No.	0.00085;				
Matches	34;	Conservative	20;	Mismatches	52;	Indels	16;
Qy	6	LEVLVAGAGLENTDYL	CNMDPYAILKCRSQKSS	IATGKGT-TP	EWNNFIF	-----	58
Db	62	LRCVMYQARDLAAMD	KDSFSDPYAIVSFLH	QSKTVV--KNT	LNPTWDQTLIF	YEIEIF	119
Qy	59	-----TVSDRTD	LVIKLMDSDTG	TADDFVGEATIP	LEAVYTERSIP	PTLYNVVKG	KYCG 114
Db	120	GEPATVAEQPPSI	WELVDYDHTYGADEF	MGRCCIQPS---L	ERMPLIAFP	FLTRGSP	QPSG 176
Qy	115	EI	116				
Db	177	EL	178				

RESULT 5
 US-09-382-552-2
 ; Sequence 2, Application US/09382552
 ; Patent No. 6673909
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Jr., Robert H.
 ; APPLICANT: Liu, Jing
 ; APPLICANT: Aoki, Masashi
 ; APPLICANT: Ho, Meng
 ; APPLICANT: Matsuda-Asada, Chie
 ; TITLE OF INVENTION: DYSPERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
 ; TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
 ; FILE REFERENCE: 00786/399002
 ; CURRENT APPLICATION NUMBER: US/09/382,552
 ; CURRENT FILING DATE: 1999-08-25
 ; EARLIER APPLICATION NUMBER: US 60/097,927

; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2080
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-552-2

Query Match 14.0%; Score 106; DB 4; Length 2080;
Best Local Similarity 27.9%; Pred. No. 0.0025;
Matches 34; Conservative 20; Mismatches 52; Indels 16; Gaps 4;
Qy 6 LEVLLVGAKGLENLDYLCNMDPYAILKCRSQEQKSSATGKGT-TPEWNNFIF-----58
Db 1154 LRCYMQARDLAAMDKDSFDPYAIVSLHQSQTVVV--KNTLNPTWDQTLIFVEIEIF 1211
Qy 59 ----TVSDRTDVLVILKMSDTGTADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKCG 114
Db 1212 GEPATVAEQPPSIVVELYDHDYGADEFMGRICQPS---LERMPRLAWFPLTRGSQPSG 1268
Qy 115 EI 116
Db 1269 EL 1270

RESULT 6

US-09-382-552-88
; Sequence 88, Application US/09382552
; Patent No. 6673909
; GENERAL INFORMATION:
; APPLICANT: Brown, Jr., Robert H.
; APPLICANT: Liu, Jing
; APPLICANT: Aoki, Masashi
; APPLICANT: Ho, Meng
; APPLICANT: Matsuda-Asada, Chie
; TITLE OF INVENTION: DYSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
; TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
; FILE REFERENCE: 00786/399002
; CURRENT APPLICATION NUMBER: US/09/382,552
; EARLIER FILING DATE: 1993-08-25
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-382-552-88

Query Match 13.8%; Score 104.5; DB 4; Length 82;
Best Local Similarity 35.7%; Pred. No. 3.4e-05;
Matches 25; Conservative 13; Mismatches 19; Indels 13; Gaps 3;
Qy 26 DPYAIVLKRSEQKSSATGKGT-TPEWNNFIF-----TVSDRTDVLVILKMS 74
Db 15 DPYAIVSLHQSQTVVV--KNTLNPTWDQTLIFVEIEIFGEPATVAEQPPSIVVELYDH 72
Qy 75 DTGTADDFVG 84
Db 73 DTGADEFMG 82

RESULT 7

US-08-909-954-4
; Sequence 4, Application US/08909954A
; Patent No. 6100058
; GENERAL INFORMATION:
; APPLICANT: Allen, Maxine J.
; APPLICANT: Buckler, Alan J.
; TITLE OF INVENTION: GAP12 Genes and their Uses
; FILE REFERENCE: SEQ-11p

; CURRENT APPLICATION NUMBER: US/08/909,954A
; CURRENT FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 799
; TYPE: PRT
; ORGANISM: M. musculus
US-08-909-954-4

Query Match 13.8%; Score 104.5; DB 3; Length 799;
Best Local Similarity 23.4%; Pred. No. 0.00096;
Matches 36; Conservative 26; Mismatches 67; Indels 25; Gaps 4;
Qy 4 GTLEVLVGAKGLENLDYLCNMDPYAILKCRSQEQKSSATGKGTTPWNNENPIFTVSDR 63
Db 5 GSLSIRVEGRALPAKDVSGSDPYCLVKVDQDVARTATWRSLSFPWGEETVHLPLD 64
Qy 64 TTDLVILKMSDTGTADDFVGEATIPLEAVYTTERSIPPTLYNV-----VKGEKYCGE 115
Db 65 FHHLAFVVLDEDTVGDDIIIGKISLSKEAITADPRGIDSWINLSRVDPAEVQGE-VCLD 123
Qy 116 IKVGLTFPTEDTRQGL-----PEDFG 138
Db 124 VKL-----LEDARGCLRHVRQARDLAPRDISG 152

RESULT 8

US-10-092-138A-27
; Sequence 27, Application US/10092138A
; Patent No. 6743630
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/092,138A
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 672
; TYPE: PRT
; ORGANISM: human
US-10-092-138A-27

Query Match 13.6%; Score 102.5; DB 4; Length 672;
Best Local Similarity 30.6%; Pred. No. 0.0013;
Matches 37; Conservative 14; Mismatches 49; Indels 21; Gaps 5;
Qy 6 LEVLLVGAKGLENLDYLCNMDPYAILKCR-----RSQEQKSSATGKGT-TPEWNNENPIFTV- 60
Db 173 LHVTVDRADKGLIPMDPNGLSDPYVKULIPDPKNESKQTKTIRSTLNPNWNESFTPLK 232
Qy 61 -SDRTDVLVILKMSDTGTADDFVGEAT-----IPLEAVYTTERSIPPTLYNVVKGK 111
Db 233 PSDKDRRLSVEIWDWDRTTTENDFMGSLSCFVSELKMKMPASGWY-----KLLNQEGEY 285
Qy 112 Y 112
Db 286 Y 286

RESULT 9

US-09-538-092-943
; Sequence 943, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092

;
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 943
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P17252
US-09-538-092-943

Query Match 13.6%; Score 102.5; DB 4; Length 672;
Best Local Similarity 30.6%; Pred. No. 0.0013;
Matches 37; Conservative 14; Mismatches 49; Indels 21; Gaps 5;

QY 6 LEVLVGAAGLENTDYLGNMPPYAILKC-----RSQEQKSSIAATGKT-TPEWNNENFIFTV- 60
Db 173 LHVTVRDAKNLIPMDPNGLSDPYVKLIPDPKNSKQKTKTIRSTLNQWNESFTFKLK 232
QY 61 -SDRTTDLVIKLDSDTGTADDVFGAET-----IPLAVYTERSIPPTLYNVVKGK 111
Db 233 PSKDRRLSVEIWDWDRTRTRNDFMGLSFGVSELMKMPASGWY-----KLLNQBEGBY 285

QY 112 Y 112
Db 286 Y 286

RESULT 10
US-09-248-796A-18185
; Sequence 18185, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18185
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18185

Query Match 13.2%; Score 99.5; DB 4; Length 233;
Best Local Similarity 33.3%; Pred. No. 0.00065;
Matches 23; Conservative 12; Mismatches 33; Indels 1; Gaps 1;

QY 5 TLEVLVGAAGLENTDYLGNMPPYAILKCRSQEQKSSIAATGKTTPWNNENFIFTVSDRT 64
Db 17 TINVKVAAESLYKRDVFRQDPDFAVLTVDGSGTKTTITAKTLNPNWNETNFQAKDS 76

QY 65 TDLVIKLD 73
Db 77 I-LVIQVDF 84

RESULT 11
US-09-417-197-73
; Sequence 73, Application US/09417197
; Patent No. 6518021

;
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion construct
US-09-417-197-73

Query Match 12.9%; Score 97.5; DB 4; Length 916;
Best Local Similarity 26.4%; Pred. No. 0.0086;
Matches 32; Conservative 20; Mismatches 48; Indels 21; Gaps 4;

QY 6 LEVLVGAAGLENTDYLGNMPPYAILKC-----RSQEQKSSIAATGKTTPWNNENFIFTV- 60
Db 173 LHVTVRDAKNLIPMDPNGLSDPYVKLIPDPKNSKQKTKTIRSTLNQWNESFTFKLK 232
QY 61 -SDRTTDLVIKLDSDTGTADDVFGAET-----IPLAVYTERSIPPTLYNVVKGK 111
Db 233 PSKDRRLSVEIWDWDRTRTRNDFMGLSFGVSELMKMPASGWY-----KAHQBEGBY 285

QY 112 Y 112
Db 286 Y 286

RESULT 12
US-09-270-767-43037
; Sequence 43037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43037
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43037

Query Match 12.8%; Score 96.5; DB 4; Length 172;
Best Local Similarity 28.0%; Pred. No. 0.00098;
Matches 40; Conservative 18; Mismatches 66; Indels 19; Gaps 6;

QY 16 LENTDYLGNMPPYAILKCRSQEQKSSI-----ATGKGT-TPEWNNENFIFTVSDRTDLVI 69
Db 2 LAKKDIFGASDPYVRIDLNTINGDINIDSVLTTKTKKTLNPTWNEEFIFRVKPSHKLVF 61
QY 70 KLMSDTCGTADDVFGCAITPLEAVYTE---RSIPPTLY-----NVVKGKCYGEIKVGL 120
Db 62 QVFENRILTRDDFLGNVELTLVNLPTFQEGRTIGEQSTLPRRSVGAKSRIKGLIRIYH 121

QY 121 TFTPEDTTRQGLP---EDFGGK 140
Db 122 AFIRE-TREQSEPPSSGNSDGEWE 143

RESULT 13
US-08-539-205A-4
; Sequence 4, Application US/08539205A
; Patent No. 6001619

```
;
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Caligiuri, Maureen
; APPLICANT: Nefsky, Bradley
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,205A
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSV-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-539-205A-4

Query Match 12.8%; Score 96.5; DB 3; Length 766;
Best Local Similarity 32.4%; Pred. No. 0.0088;
Matches 22; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSSATGKTTPWNNENFIFTVSORTT 65
Db 10 IRVTIVAADGLYKRDVFRFPDPFAVLTVDSGEQTHHTTAIKKTLNPNWNETFEVNVTONST 69
Qy 66 DLVIKLM 73
Db 70 -IAIQVFD 76

RESULT 14
US-09-392-163A-4
; Sequence 4, Application US/09392163A
; Patent No. 6503742
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Caligiuri, Maureen
; APPLICANT: Nefsky, Bradley
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,163A
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;
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/539,205
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSV-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-392-163A-4

Query Match 12.8%; Score 96.5; DB 4; Length 766;
Best Local Similarity 32.4%; Pred. No. 0.0088;
Matches 22; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKCRSQEQKSSATGKTTPWNNENFIFTVSORTT 65
Db 10 IRVTIVAADGLYKRDVFRFPDPFAVLTVDSGEQTHHTTAIKKTLNPNWNETFEVNVTONST 69
Qy 66 DLVIKLM 73
Db 70 -IAIQVFD 76

RESULT 15
US-09-538-092-853
; Sequence 853, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 853
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P05127
; US-09-538-092-853

Query Match 12.7%; Score 96; DB 4; Length 673;
Best Local Similarity 26.7%; Pred. No. 0.0084;
Matches 32; Conservative 17; Mismatches 47; Indels 24; Gaps 3;

Qy 6 LEVLLVGAKGLENTDYLCNMDPYAILKC-----RSQKSSATGKTTPWNNENFIFTV- 60
Db 173 LVLVRDAKNLVPMDFNGLSDPYVKLIPDPKSESQKTKTKCSLNPNWNETFRFLK 232
Qy 61 -SDRTTDLVIKLMDSDTGTADDFVGRATIPL-----BAVYTERSIPT 101
Db 233 ESDKDRRLSVEIWDWDLTSRDNDFMGLSLSGISLQKASVDGWFKLISQEGEYFNVVPP 292

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Job time : 43 secs

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-913-569B-6
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Sequence: 1 MVHGTLEVLVGAGKLENTD.....PEDTRQGLPEDFGMKQSS 143

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Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pap.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	100.0	143	17	US-10-425-115-329461 Sequence 329461,
2	756	100.0	177	15	US-10-425-114-37991 Sequence 37991, A
3	605.5	80.1	144	16	US-10-437-963-198977 Sequence 198977,
4	574.5	76.0	144	17	US-10-425-115-337424 Sequence 337424,
5	523	69.2	155	15	US-10-425-114-60607 Sequence 60607, A
6	496	65.6	242	17	US-10-425-115-351774 Sequence 351774,
7	482	63.8	151	16	US-10-437-963-144023 Sequence 144023,
8	465.5	61.6	136	16	US-10-767-701-42740 Sequence 42740, A
9	465	61.5	144	17	US-10-425-115-196450 Sequence 196450,
10	465	61.5	144	17	US-10-425-115-291094 Sequence 291094,
11	460.5	60.9	143	17	US-10-425-115-196454 Sequence 196454,
12	455	60.2	167	16	US-10-437-963-189521 Sequence 189521,
13	427	56.5	141	17	US-10-425-115-307041 Sequence 307041,

14	404.5	53.5	149	15	US-10-425-114-46233 Sequence 46233, A
15	300.5	39.7	153	15	US-10-424-599-220600 Sequence 220600,
16	288.5	38.2	155	16	US-10-767-701-32195 Sequence 32195, A
17	282.5	37.4	157	17	US-10-425-115-349731 Sequence 349731,
18	271.5	35.9	151	15	US-10-424-599-253644 Sequence 253644,
19	262.5	34.7	134	17	US-10-425-115-192911 Sequence 192911,
20	246.5	32.6	159	16	US-10-437-963-145889 Sequence 145889,
21	219	29.0	69	16	US-10-437-963-135864 Sequence 135864,
22	208.5	27.6	114	17	US-10-425-115-280877 Sequence 280877,
23	168	22.2	67	15	US-10-424-599-236750 Sequence 236750,
24	163	21.6	80	15	US-10-424-599-279237 Sequence 279237,
25	163	21.6	263	17	US-10-739-930-7139 Sequence 7139, Ap
26	154.5	20.4	756	16	US-10-437-963-194126 Sequence 194126,
27	150	19.8	258	15	US-10-424-599-176931 Sequence 176931,
28	150	19.8	278	15	US-10-425-114-68284 Sequence 68284, A
29	146.5	19.4	140	15	US-10-424-599-277634 Sequence 277634,
30	144	19.0	272	17	US-10-739-930-10107 Sequence 10107, A
31	143.5	19.0	370	16	US-10-767-701-42589 Sequence 42589, A
32	143.5	19.0	444	17	US-10-425-115-302132 Sequence 302132,
33	141	18.7	130	15	US-10-424-599-215673 Sequence 215673,
34	139.5	18.5	575	16	US-10-437-963-116289 Sequence 116289,
35	136.5	18.1	565	16	US-10-437-963-168257 Sequence 168257,
36	135.5	17.9	145	17	US-10-425-115-353108 Sequence 353108,
37	135.5	17.9	670	16	US-10-437-963-194703 Sequence 194703,
38	134.5	17.8	221	16	US-10-767-701-35093 Sequence 35093, A
39	133.5	17.7	438	15	US-10-425-114-66696 Sequence 66696, A
40	133.5	17.7	580	17	US-10-425-115-216663 Sequence 216663,
41	133.5	17.7	1067	16	US-10-437-963-142010 Sequence 142010,
42	133	17.6	268	15	US-10-424-599-163344 Sequence 163344,
43	131	17.3	539	15	US-10-424-599-243822 Sequence 243822,
44	130.5	17.3	286	17	US-10-425-115-274891 Sequence 274891,
45	130.5	17.3	288	17	US-10-425-115-274888 Sequence 274888,

ALIGNMENTS

RESULT 1
US-10-425-115-329461
; Sequence 329461, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 329461
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_63541C.1.pep
US-10-425-115-329461

Query Match	100.0%	Score	756	DB	17	Length	143
Best Local Similarity	100.0%	Pred. No.	1e-75				
Matches	143	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MVHGTLEVLVGAGKLENTDYLNCMDPYAILKCRSQSKSIATGKGTTPWNNFIPTV	60				
Db	1	MVHGTLEVLVGAGKLENTDYLNCMDPYAILKCRSQSKSIATGKGTTPWNNFIPTV	60				
Qy	61	SDRTDLVILMDSDTGTTADDFGEATIPLEAVYTERSIPPTLYNVVKGKCCGEIKVGL	120				
Db	61	SDRTDLVILMDSDTGTTADDFGEATIPLEAVYTERSIPPTLYNVVKGKCCGEIKVGL	120				
Qy	121	TFTPEDTRQGLPEDFGMKQSS	143				

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|||||
Db 121 TFTPEDTRQGLPEDFGWKQSS 143

RESULT 2
US-10-425-114-37991
; Sequence 37991, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37991
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-020-C12_FLI.pep
US-10-425-114-37991

Query Match 100.0%; Score 756; DB 15; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSATGKGTTPENWENFIFTV 60
Db 35 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSATGKGTTPENWENFIFTV 94
QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGEIKVGL 120
Db 95 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGEIKVGL 154
QY 121 TFTPEDTRQGLPEDFGWKQSS 143
Db 155 TFTPEDTRQGLPEDFGWKQSS 177

RESULT 3
US-10-437-963-198977
; Sequence 198977, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198977
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94586C.1.pep
US-10-437-963-198977

Query Match 80.1%; Score 605.5; DB 16; Length 144;
Best Local Similarity 79.9%; Pred. No. 5.6e-59;
Matches 115; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSATGKGTTPENWENFIFTV 60
Db 1 MVQGTLEVLVGAAGLENTDYLNNMDPYAVLKCRSQEQKSSVASKGSDPENWETPMFSV 60
QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGEIKVGL 120
Db 61 THNATELIKLMDSGTDGDDFVGEATISLEAIYTEGSIPTPTVYVNVKDEEYRGEIKVGL 120
QY 121 TFTPEDTRQGL-PEDFGWKQSS 143
Db 121 TFTPEDTRQGLSEEDIGWKQSS 144

RESULT 4
US-10-425-115-337424
; Sequence 337424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337424
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70901C.1.pep
US-10-425-115-337424

Query Match 76.0%; Score 574.5; DB 17; Length 144;
Best Local Similarity 74.3%; Pred. No. 1.6e-55;
Matches 107; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY 1 MVHGTLEVLVGAAGLENTDYLNNMDPYAILKCRSQEQKSSATGKGTTPENWENFIFTV 60
Db 1 MAQGTLEVLVGAAGLENTDYLNNMDPYAVLKCRSQEQKSTVASKGSDPENWETPMFTV 60
QY 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTERSIPPTLYNVVKGKCYGEIKVGL 120
Db 61 SENATELVKLLDSGGTDDSVGEATIPDGVYTEGSIPTPTVYVNVKDEEYRGEIKVGL 120
QY 121 TFTPEDTRQGLPED-FGKWQSS 143
Db 121 TFTPEDTRQGLPEENYGGWQSS 144

RESULT 5
US-10-425-114-60607
; Sequence 60607, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60607
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3597-068-A11_FLI.pep
US-10-425-114-60607

Query Match          69.2%; Score 523; DB 15; Length 155;
Best Local Similarity 78.6%; Pred. No. 9.3e-50;
Matches 99; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MVHGTLEVLVGAKGLNTDYLNMDPYAILKCRSQKSIATGKGTTPWNNFTFV 60
Db 27 MAQGTLEVLVGARGLENTDYLNMDPYALLQCRSHQKSSVASGKCEPEWNETFVFTV 86

Qy 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYGCEIKVGL 120
Db 87 SDGAAELFIKLLSDSGTDDDFVGEATIPLEAVYTTEGNIPTTVYVNVVKDEYRGEIKVGL 146

Qy 121 TFTPED 136
Db 147 TFTPED 152

RESULT 6
US-10-425-115-351774
; Sequence 351774, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351774
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(242)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_83984C.1.pep
US-10-425-115-351774

Query Match          65.6%; Score 496; DB 17; Length 242;
Best Local Similarity 61.9%; Pred. No. 1.7e-46;
Matches 99; Conservative 11; Mismatches 16; Indels 34; Gaps 1;

Qy 1 MVHGTLEVLVGAKGLNTDYLNMDPYAILKCRSQKSIATGKGTTPWNNFTFV 60
Db 80 MAQGTLEVLVGARGLENTDYLNMDPYALLQCRSHQKSSVASGKCEPEWNETFVFTV 139

Qy 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYGCEIKVGL 120
Db 140 SDGAAELFIKLLSDSGTDDDFVGEATYXRLSSAYLSLYNLNLSLHGLYQLLIIVLS 199

Qy 88 -IPLEAVYTTERSIPPTLYNVVKGKYGCEIKVGLTFTPED 126
Db 200 QIPLEAVYTTEGNIPTTVYVNVVKDEYRGEIKVGLTFTPED 239

RESULT 7
US-10-437-963-144023
; Sequence 144023, Application US/10437963
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437.963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144023
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44875C.1.pep
US-10-437-963-144023

Query Match          63.8%; Score 482; DB 16; Length 151;
Best Local Similarity 62.7%; Pred. No. 3.2e-45;
Matches 94; Conservative 10; Mismatches 14; Indels 32; Gaps 1;

Qy 25 MDPYAILKCRSQKSSSIAT-----GKGTTPW 52
Db 1 MDPYAILKCRSQKSSSIASVLWCIADEWNDLTVRIIPKECIAMCNFCYVDCGKSNPEW 60

Qy 53 NENFIFTVSDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYG 112
Db 61 NENFVPVSDKATELILKLLASDTGSPDDFVGEATIPLEPYTEGSIPTPLYNVVKDDHS 120

Qy 113 CGBIKVGLTFTPTEDTRQGLPEDFGGWKQS 142
Db 121 CGBIKVGLPFPEDVRQGLPEDFGGWKQS 150

RESULT 8
US-10-767-701-42740
; Sequence 42740, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767.701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42740
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C15003_1.pep
US-10-767-701-42740

Query Match          61.6%; Score 465.5; DB 16; Length 136;
Best Local Similarity 68.4%; Pred. No. 1.9e-43;
Matches 93; Conservative 15; Mismatches 23; Indels 5; Gaps 3;

Qy 1 MVHGTLEVLVGAKGLNTDYLNMDPYAILKCRSQKSIATGKGTTPWNNFTFV 60
Db 1 MVHGTLEVLVSAKGLDFTDLNNMDFVLTCTQEQKSSVANGAGSEPEWNETFVFTV 60

Qy 61 SDRTTDLVIKLMDSGTGADDFVGEATIPLEAVYTTERSIPPTLYNVVKGKYGCEIKVGL 120
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; SEQ ID NO 189521
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86022C.1.pap
US-10-437-963-189521

Query Match      60.2%; Score 455; DB 16; Length 167;
Best Local Similarity 62.9%; Pred. No. 3.7e-42;
Matches 90; Conservative 15; Mismatches 26; Indels 12; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MVHGKLEVLVCAKGLDTEFLNDMDPYVILTCRSEQSVAKGAGSEPEWNETFFVTV 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVGL 120
Db 61 SDDVPQLNVKIMDSNAPSADDFVGEANIPLEPVFLEGLSPPAVHRVVKBEKCYGKIKVAL 120

Qy 121 TFTP-----EDTRQG 131
Db 121 TFTPAAETRRHHNHNENEGTRTG 143

RESULT 13
US-10-425-115-307041
; Sequence 307041, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 307041
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43093C.1.pap
US-10-425-115-307041

Query Match      56.5%; Score 427; DB 17; Length 141;
Best Local Similarity 56.6%; Pred. No. 3.8e-37;
Matches 81; Conservative 23; Mismatches 37; Indels 2; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MVRGKLEVLVSAKGLDSDFFNSMDPYVILTCRSEQSVASGAGSEPEWNETFFPAI 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVGL 120
Db 61 SGDAPELRVKIMDSALSDADLVGEACIPLEAVLQEGSLPPAVHRVVKDBEYRGEIKIAL 120

Qy 121 TFTPEDTRQRLPEDFGWKQSS 143
Db 121 TFTPABENEE--ESYGMNQST 141

RESULT 14
US-10-425-114-46233
; Sequence 46233, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46233
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701130512_FLI.pap
US-10-425-114-46233

Query Match      53.5%; Score 404.5; DB 15; Length 149;
Best Local Similarity 52.1%; Pred. No. 1.3e-36;
Matches 76; Conservative 29; Mismatches 38; Indels 3; Gaps 1;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MPRGTLEVLVISAKGIDDDNFLSSIDPVILTYRAQEKSTVQEDAGSKPQWNESEFLTV 60

Qy 61 SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGKCYGKIKVGL 120
Db 61 SDSASELNLKIMDKDNFSQDDCLGEATIHLDVPFEAGSIPETAYKVVKDBEYCGEIKVAL 120

Qy 121 TFTPEDTRQRL---PEDFGWKQSS 143
Db 121 TFTAERNEEQYDAPBESYGMWKESS 146

RESULT 15
US-10-424-599-220600
; Sequence 220600, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220600
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41232C.1.pap
US-10-424-599-220600

Query Match      39.7%; Score 300.5; DB 15; Length 153;
Best Local Similarity 42.5%; Pred. No. 4.9e-25;
Matches 65; Conservative 30; Mismatches 45; Indels 13; Gaps 4;

Qy 1 MVHGTLEVLVAGKGLNTDYLNCMDPYAILKCRSQKSSSIATGKGTTPWNNENFIPTV 60
Db 1 MAIGPNEVLVAKGLQETDIFAHMDPYVLLQYQGERKSSSVIHEGGRNFINWKEKFFRV 60

Qy 61 ----SDRTTDLVIKLMDSDTGADDFVGEATIPLEAVYTERTSIPPTLYNVVKGK 110
Db 61 EYPGSGDQYKLNIRIMDKDVSADDFVQATIVVKOLLAEGAENGSAELRPHKYSVVVRAD 120

Qy 111 K-YCGEIKVGLTFTPTEDTRQRLPEDFGWKQSS 142
Db 121 QSYCGEIEVGITPTRKE--EEYIEDDVGGWKES 151
```

Search completed: January 6, 2005, 14:15:34
Job time : 150 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2005, 13:25:47 ; Search time 194 Seconds
(without alignments)
424.116 Million cell updates/sec

Title: US-09-913-569B-6

Perfect score: 756

Sequence: 1 MVHGTLEVLVAGKGLNTD.....PEDTRQGLPEDFGWKQS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	91.0	143	2 Q6H7E3	Q6H7E3 oryza sativ
2	605.5	80.1	144	2 Q82550	Q82550 oryza sativ
3	605.5	80.1	144	2 Q7F9X0	Q7F9X0 oryza sativ
4	605.5	80.1	144	2 CAE03867	CAE03867 oryza sat
5	486.5	64.4	147	2 Q9C886	Q9C886 arabidopsis
6	483.5	64.0	147	2 Q8LDR6	Q8LDR6 arabidopsis
7	455.5	60.3	143	2 Q24582	Q24582 zea mays (m
8	455	60.2	128	2 Q9SMH6	Q9SMH6 zea mays (m
9	454.5	60.1	145	2 Q7XPW6	Q7XPW6 oryza sativ
10	393.5	52.1	143	2 Q9ZRV6	Q9ZRV6 cicer ariet
11	259	34.3	156	2 Q50006	Q50006 oryza sativ
12	259	34.3	156	2 Q7GC09	Q7GC09 oryza sativ
13	247.5	32.7	159	2 Q8LPB3	Q8LPB3 oryza sativ
14	246.5	32.6	159	2 Q50005	Q50005 oryza sativ
15	240.5	31.8	156	2 Q9M2T2	Q9M2T2 arabidopsis
16	240.5	31.8	159	2 Q7Y0Z1	Q7Y0Z1 oryza sativ
17	232	30.7	151	2 Q8S2B8	Q8S2B8 oryza sativ
18	186	24.6	137	1 P16B_CUCMA	Q9ZT46 cucurbita m
19	179	23.7	254	2 Q9U7P0	Q9U7P0 eufolliculi
20	177	23.4	149	1 P16A_CUCMA	Q9ZT47 cucurbita m
21	166	22.0	247	2 Q945K9	Q945K9 arabidopsis
22	166	22.0	247	2 AA741866	AA741866 arabidops
23	155	20.5	595	2 Q9SDM4	Q9SDM4 dunaliella
24	151	20.0	953	2 Q7PTC2	Q7PTC2 anopheles g
25	149.5	19.8	1020	2 Q9ZVT9	Q9ZVT9 arabidopsis
26	146.5	19.4	221	2 Q6ES10	Q6ES10 oryza sativ
27	145	19.2	279	2 Q49490	Q49490 arabidopsis
28	139.5	18.5	575	2 Q7XTW4	Q7XTW4 oryza sativ
29	136.5	18.1	422	2 Q6U0U5	Q6U0U5 oryza sativ
30	136.5	18.1	422	2 AAQ56572	AAQ56572 oryza sat
31	136.5	18.1	565	2 Q6ZDC3	Q6ZDC3 oryza sativ

```
RESULT 1
Q6H7E3 PRELIMINARY; PRT; 143 AA.
AC Q6H7E3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative elicitor-responsive gene-3.
GN Name=P0010C01.27;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AP004768; BAD25356.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_GaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
SQ SEQUENCE 143 AA; 15776 MW; B82566661199B39E6 CRC64;

Query Match 91.0%; Score 688; DB 2; Length 143;
Best Local Similarity 89.4%; Pred. No. 7e-61;
Matches 127; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MVHGTLEVLVAGKGLNTDYLGNMDDPYAILKCRSQSKSIATGKTTPWNNFVFTV 60
Db 1 MVHGTLEVLVAGKGLNTDYLGNMDDPYAILKCRSQSKSIATGKTTPWNNFVFTV 60
Qy 61 SDRTDLIVIKLMDSDTADDFVGEATIPLEAVYTERSIPPTLYNVVKGYKCGEIKVGL 120
Db 61 SDKATELLIKLSDSDTADDFVGEATIPLEAVYTERSIPPTLYNVVKDEHYCCEIKVGL 120
Qy 121 TPTPEDTRQGLPEDFGWKQS 142
Db 121 TPTPEDVRQGLPEDFGWKQS 142

RESULT 2
Q82550 PRELIMINARY; PRT; 144 AA.
AC Q82550;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DE Putative elicitor-responsive gene-3.
GN Name=ERG3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sakaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AP004768; BAD25356.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_GaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
SQ SEQUENCE 143 AA; 15776 MW; B82566661199B39E6 CRC64;

Query Match 91.0%; Score 688; DB 2; Length 143;
Best Local Similarity 89.4%; Pred. No. 7e-61;
Matches 127; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MVHGTLEVLVAGKGLNTDYLGNMDDPYAILKCRSQSKSIATGKTTPWNNFVFTV 60
Db 1 MVHGTLEVLVAGKGLNTDYLGNMDDPYAILKCRSQSKSIATGKTTPWNNFVFTV 60
Qy 61 SDRTDLIVIKLMDSDTADDFVGEATIPLEAVYTERSIPPTLYNVVKGYKCGEIKVGL 120
Db 61 SDKATELLIKLSDSDTADDFVGEATIPLEAVYTERSIPPTLYNVVKDEHYCCEIKVGL 120
Qy 121 TPTPEDTRQGLPEDFGWKQS 142
Db 121 TPTPEDVRQGLPEDFGWKQS 142

RESULT 2
Q82550 PRELIMINARY; PRT; 144 AA.
AC Q82550;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DE Putative elicitor-responsive gene-3.
GN Name=ERG3;
```


[illegible]

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid1; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OC NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Etolated epicotyls;
 RA Duplco B., Esteban R., Labrador E.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 DR EMBL; AJ012692; CAA10133.1; -.
 DR HSSP; P05696; 1DSY.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLB.
 DR Pfam; PF00168; C2; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR SMART; SM00239; C2; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 KW Hypothetical protein
 SQ SEQUENCE 143 AA; 16091 MW; 64ED12D3671B4732 CRC64;
 Query Match 52.1%; Score 393.5; DB 2; Length 143;
 Best Local Similarity 51.7%; Pred. No. 2.4e-31;
 Matches 74; Conservative 27; Mismatches 39; Indels 3; Gaps 1;
 QY 1 MHGTELVLLVGAKLENTDYLNCMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 60
 DB 1 MPRGTLEVLLSARGLDNDLSSIDPYVILSYRAQEHKSTVQEGAGSNPQWNETFLFTV 60
 QY 61 SDRTTDLVILKMDSDTGTADDFVGEATIPLEAVYTERSIPPTLYNVVKGK-Y 120
 DB 61 SDSASELNLRIEMKDNFNNDNLGEALIPLEAVFEGSLAENYKLVKEQYCGEIKVAL 120
 QY 121 TFTPEDTRQGLPDPFGGWKQSS 143
 DB 121 TFTPENDEE---ETCGGWKEST 140
 RESULT 11
 ID O50006 PRELIMINARY; PRT; 156 AA.
 AC O50006;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Os-FIERG2 protein.
 GN Name=Os-FIERG2;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim C.-Y., Choe M.S., Jeong S.-Y., Bae C.-G., Cheong Y.H., Han C.-D.,
 RA Cho M.-J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 DR EMBL; U95136; AAC04628.1; -.
 DR PIR; T04363; T04363.
 DR HSSP; P04410; 1A25.
 DR Gramene; O50006; -.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLB.
 DR Pfam; PF00168; C2; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR SMART; SM00239; C2; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 SQ SEQUENCE 156 AA; 17436 MW; 63EAB8006CBA2D90 CRC64;
 Query Match 34.3%; Score 259; DB 2; Length 156;
 Best Local Similarity 41.3%; Pred. No. 8.1e-18;
 Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;
 QY 4 GTLEVLVLVGAKLENTDYLNCMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
 DB 5 GVLEVLVLDAKGLTGNDFLGKIDPYVVVQVRSQKRSVARDQGNPSWNEVFKFQINST 64
 QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNVVKGK-Y 112
 DB 65 AATGQHKLFLRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124
 QY 113 CGEIKVGLTFTPEDTRQGLPDPFGGWKQS 142
 DB 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153
 RESULT 13
 ID Q8LPB3 PRELIMINARY; PRT; 159 AA.
 AC Q8LPB3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RPP17-1.
 GN Name=Rpp17-1;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

QY 4 GTLEVLVLVGAKLENTDYLNCMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
 DB 5 GVLEVLVLDAKGLTGNDFLGKIDPYVVVQVRSQKRSVARDQGNPSWNEVFKFQINST 64
 QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNVVKGK-Y 112
 DB 65 AATGQHKLFLRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124
 QY 113 CGEIKVGLTFTPEDTRQGLPDPFGGWKQS 142
 DB 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153
 RESULT 12
 ID Q7GC09 PRELIMINARY; PRT; 156 AA.
 AC Q7GC09;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RPP17-2.
 GN Name=Rpp17-2;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22086689; PubMed=12091721;
 RA Asano T., Kusano H., Okuda T., Kubo N., Shimada H., Kadowaki K.;
 RA "Rpp16 and Rpp17, from a common origin, have different protein
 RT characteristics but both genes are predominantly expressed in rice
 RT phloem tissues";
 RL Plant Cell Physiol. 43:668-674 (2002).
 CC -1- SIMILARITY: Contains 1 C2 domain.
 DR EMBL; AB060730; BAC06446.1; -.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLB.
 DR Pfam; PF00168; C2; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR SMART; SM00239; C2; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 SQ SEQUENCE 156 AA; 17436 MW; 63EAB8006CBA2D90 CRC64;
 Query Match 34.3%; Score 259; DB 2; Length 156;
 Best Local Similarity 41.3%; Pred. No. 8.1e-18;
 Matches 62; Conservative 22; Mismatches 54; Indels 12; Gaps 4;
 QY 4 GTLEVLVLVGAKLENTDYLNCMDPYAILKCRSQKSIATGKGTTPWNNFTVSDR 63
 DB 5 GVLEVLVLDAKGLTGNDFLGKIDPYVVVQVRSQKRSVARDQGNPSWNEVFKFQINST 64
 QY 64 TT----DLVIKLMDSDTGTADDFVGEAT-----IPLEAVYTERSIPPTLYNVVKGK-Y 112
 DB 65 AATGQHKLFLRLMDHDTFSRDDFLGEATINVTDLISLGMHGTWEMSESXKRVVLADKTY 124
 QY 113 CGEIKVGLTFTPEDTRQGLPDPFGGWKQS 142
 DB 125 HGEIRVSLTFT-ASAKAQDHAEQVGWNAHS 153
 RESULT 13
 ID Q8LPB3 PRELIMINARY; PRT; 159 AA.
 AC Q8LPB3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RPP17-1.
 GN Name=Rpp17-1;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OX Ehrhartoideae; Oryzeae; Oryza.
RN [1] NCBI_TaxID=39947;
RP SEQUENCE FROM N.A.
RX MEDLINE=22086689; PubMed=12091721;
RA Asano T., Kusano H., Okuda T., Kubo N., Shimada H., Kadowaki K.;
RT "Rp16 and Rp17, from a common origin, have different protein
RT characteristics but both genes are predominantly expressed in rice
RT phloem tissues.";
RL Plant Cell Physiol. 43:668-674(2002).
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AB060730; BAC06445.1; -.
DR HSSP; P04110; 1A25.
DR Gramine; O8LPB3.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ SEQUENCE 159 AA; 1736 MW; 84FD85B5AD62D59 CRC64;

Query Match
Best Local Similarity 32.7%; Score 247.5; DB 2; Length 159;
Matches 62; Conservative 22; Mismatches 54; Indels 15; Gaps 5;

QY 4 GTLEVLVGAAGLENTDYL---CNMDPYAILKCRSQEQKSSSTATGKTTPEWNEFIPTV 60
DB 5 GVLEHLVDAGKLTGNDLGEIGNHPYVVQYRSQERKSSVARDDGKNPNSNEVFKFQI 64
QY 61 SDRTT---DLVIKLMDSDTGTDADFVGEAT-----IPLEAVYTTERSIPPTLYNVVKG 110
DB 65 NSTAATGQHKLFRLMDHDTFSRDDFLGEATINVTDLISLGHGHTWEMSESKHRVVLAD 124
QY 111 K-YCGEIKVGLTFTPTDTRQGLPEDFGGWKQS 142
DB 125 KTYHGEIRVSLTFT-ASAKAQDHAEQVGWGAHS 156

RESULT 15
QWMT2
ID Q9M2T2 PRELIMINARY; PRT; 156 AA.
AC Q9M2T2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative elicitor responsive/phloem.
GN Name=T2E16.130; Synonyms=At3G55470/T2E16_130;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Wurmbach E., Drzonek H., Ansoerge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Ouetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Iehida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AL132975; CAB75905.1; -.
DR EMBL; AK117139; BAC41817.1; -.
DR PIR; T47686; T47686.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR NCBI_TaxID=4530;
SQ SEQUENCE 156 AA; 17316 MW; CC7FAF03D60639B CRC64;

Query Match
Best Local Similarity 31.8%; Score 240.5; DB 2; Length 156;
Matches 55; Conservative 33; Mismatches 52; Indels 15; Gaps 6;

QY 1 MVHGTLEVLVGAAGLENTDYLNCNMDPYAILKCRSQEQKSSIA-TCKGTTPEWNEFIPTV 56
DB 1 MAVGILEVLSISGKLGKRSDFLGKIDPYVEIQYKQTRKSSVAKEDGGRNPTWNDKLKWR 60
QY 57 -IFTVSDRTTDLVIKLMDSDTGTDADFVGEATIPLEAVYT-----ERSIPTLYNVVKG 109
DB 61 AEFPGSGADYKLIVKMDHDTFSDDDFIGEATVHVKELLEMGVEKGTAEIPLRPTKYNIVDS 120
QY 110 E-KYCGEIKVGLTFTPTDTRQGLP-EDFGGWKQS 142
DB 121 DLSPVGEILLIGVSYSL--LQDRGMDEGEQFGGWKHS 153

Query Match
Best Local Similarity 32.6%; Score 246.5; DB 2; Length 159;
Matches 62; Conservative 22; Mismatches 54; Indels 15; Gaps 5;

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Search completed: January 6, 2005, 14:02:45
Job time : 198 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 07:53:54 ; Search time 4016 Seconds
(without alignments)
10315.183 Million cell updates/sec

Title: US-09-913-569B-5

Perfect score: 876
Sequence: 1 gcacgaggttcgttcacgcc.....tttttgatccttgaaaaa 876

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_ey.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358.4	40.9	827	8 AK120841	AK120841 Oryza sat
2	291.6	33.3	760	8 AK063584	AK063584 Oryza sat
3	290.6	33.2	710	8 AF090698	AF090698 Oryza sat
4	276.8	31.6	432	6 BD178086	BD178086 Novel pro
5	275.4	31.4	874	8 BF009547	BF009547 Triticum
6	247	28.2	247	11 BV081654	BV081654 scl239_p3
7	247	28.2	247	11 BV081655	BV081655 scl239_p3
8	247	28.2	247	11 BV109995	BV109995 PZA01487
9	247	28.2	247	11 BV109997	BV109997 PZA01487
10	246.4	28.1	248	11 BV081650	BV081650 scl239_p3
11	246.4	28.1	248	11 BV081657	BV081657 scl239_p3
12	246.4	28.1	248	11 BV109999	BV109999 PZA01487
13	246.4	28.1	248	11 BV110002	BV110002 PZA01487
14	246	28.1	246	11 BV081652	BV081652 scl239_p3
15	246	28.1	246	11 BV109993	BV109993 PZA01487
16	242	27.6	242	11 BV081651	BV081651 scl239_p3
17	242	27.6	242	11 BV109991	BV109991 PZA01487
18	242	27.6	242	11 BV109992	BV109992 PZA01487
19	237.4	27.1	239	11 BV110000	BV110000 PZA01487

20	236.8	27.0	240	11 BV081653	BV081653 scl239_p3
21	236.8	27.0	240	11 BV109994	BV109994 PZA01487
22	231	26.4	231	11 BV081656	BV081656 scl239_p3
23	231	26.4	231	11 BV109998	BV109998 PZA01487
24	222	25.3	222	11 BV081649	BV081649 scl239_p3
25	222	25.3	222	11 BV110001	BV110001 PZA01487
26	215.6	24.6	222	11 BV110003	BV110003 PZA01487
27	198	22.6	198	11 BV110004	BV110004 PZA01487
28	197.2	22.5	667	8 BT012761	BT012761 Lycopersi
29	194.8	22.2	699	8 AK070539	AK070539 Oryza sat
30	190.2	21.7	697	8 AY085843	AY085843 Arabidops
31	190.2	21.7	726	8 AY054623	AY054623 Arabidops
32	189.4	21.6	490	8 AY081504	AY081504 Arabidops
33	178.6	20.4	695	8 BT009577	BT009577 Triticum
34	174.8	20.0	498	8 AF152601	AF152601 Zea mays
35	171.6	19.6	737	8 ZMU64437	U64437 Zea mays no
36	160	18.3	160	11 BV109996	BV109996 PZA01487
37	153	17.5	655	8 CAR012692	CAR012692 Cicer ari
38	96.4	11.0	138934	2 AP004788	AP004788 Oryza sat
39	96.4	11.0	186185	8 AP004768	AP004768 Oryza sat
40	91	10.4	483	6 A64088	A64088 Sequence 14
41	91	10.4	483	6 AX785024	AX785024 Sequence
42	79.8	9.1	3713	8 AB060729	AB060729 Oryza sat
43	79.8	9.1	65190	2 BI011H02	BI011H02 Oryza sat
44	79.8	9.1	140454	8 OSJN00183	OSJN00183 Oryza sat
45	73.4	8.4	860	8 BT009397	BT009397 Triticum

ALIGNMENTS

AK120841 827 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone: J023022G19, full insert sequence.

ACCESSION AK120841.1 GI:37990464

VERSION AK120841

KEYWORDS FLU CDNA; CAP trapper.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team.

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,

Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shiehiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group., Otono,Y., Murakami,K.,

Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Taunoda,Y., Kurotsaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,

Ikedada,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,

Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,

Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Ooato,N., Oka,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Yoshino,M. and Hayashizaki,Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

JOURNAL MEDLINE 22752273

PUBMED 12869764

REFERENCE 2

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,

Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T.,

Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Inamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,

Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hasegaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kawata, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,

Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kuroaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Nishiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Oka, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp).
Tel: 81-29-838-7007, Fax: 81-29-838-7007
This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kuroaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Haehizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oka, Y., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

Location/Qualifiers
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/mol_type="mRNA"
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/clone="001-118-A01"

TITLE JOURNAL

COMMENT

RESULT 3
AF090698
DEFINITION
Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA, complete cds.
ACCESSION
AF090698.1 GI:3603472
VERSION
AF090698.1
KEYWORDS
SOURCE
ORGANISM

LOCUS AF090698 710 bp mRNA linear PLN 16-SEP-1998
Oryza sativa elicitor-responsive gene-3 (ERG3) mRNA, complete cds.
ACCESSION AF090698
VERSION AF090698.1 GI:3603472
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 710)
AUTHORS Kim, C. Y., Cheon, S. Y., and Cho, M. J.
TITLE Identification and Characterization of Fungal Elicitor Responsive Rice Genes by mRNA Differential Display

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 710)
AUTHORS Kim, C. Y., Cheon, S. Y., and Cho, M. J.

TITLE Direct Submission
JOURNAL Submitted (04-SEP-1998) Department of Biochemistry, PMBRC, 900 Gaja-dong, Chinhae, Kyongnam 660-701, Republic of Korea

FEATURES
Location/Qualifiers
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Best Local Similarity 74.9%; Pred. No. 36-69;
Matches 393; Conservative 0; Mismatches 124; Indels 8; Gaps 2;

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107 GCCAAGGGCTCGAGAACCGATTACTCTGTAACTGATCGGTATGCAATTCCTCAAG 166
Db GCCAAGGGCTCGAGAACCGACTACTCTGTGCAACATGGACCGCTACCGGTTCTCAA 186

167 TGGCGTTACAGGAGGAGGAGGAGGATTCGCAACTGGAAGAACTACCCCTGATGG 226
Db TGGCGCTCGCAGGAGGAGGAGGAGGCTTTCGCTCAGGTAAAGATCTGACCCCTGAATGG 246

Query Match 33.2%; Score 290.6; DB 8; Length 710;
Best Local Similarity 74.9%; Pred. No. 36-69;
Matches 393; Conservative 0; Mismatches 124; Indels 8; Gaps 2;

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108	Dd	61 CAAAGGGCCTCGAACAACCGACTACTGTGTCAACATGGACCCTGACGGGTTCATAAT	120
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168	Dd	121 GCCGCTCGCAGGACGABAAGCAGCGCTGGCTCAGGTAAAGGATCTGACCCCTGAATGA	180
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228	Dd	181 ACGAAACCTTTATGTTTCAGCGTCACTCACACGGTCACAGAGCTCATCATCAAGTTGATGG	240
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288	Dd	241 ACAGTGACAGTGGCACCGATGATGTTTTGTTGGAAGCAACGATTTCTTTGGAAGCAA	300
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348	Dd	301 TCTATACAGAAGGAAGCATACCCCACTGTTTATAATGTTGTGAAGAAGAAGATATCC	360
	QY	CGCGGGAATCAAAGTTGGTCTCAATTCACCTCTGAGGATACTCGCCAGCGGGTCTCC	467
408	Dd	361 GTGGAGAAATCAAATGGGCGCTGAGTTTCACTCCAGAGGATGATCGCGATCGGGGTTTAT	420
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468	Dd	421 CTGAGGAAGACATTCGTGGATGAAGCAGTCACTTTGAGGAAGAAGCAGATACCTTTGATG	480
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520	Dd	481 TTGCAATGCAATTCGCTATGCTATGTAAGTCTGTGCTGGAAGCTCGAAC	525

RESULT 4	BD178086	432 bp	DNA	linear	PAT 16-APR-2003
LOCUS	BD178086				
DEFINITION	Novel proteins in phloem of rice and genes thereof.				
ACCESSION	BD178086				
VERSION	BD178086.1	GI:30015350			
KEYWORDS	JP 2002315582-A/1.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 432)				
AUTHORS	Kadowaki,K. and Shimada,H.				
TITLE	Novel proteins in phloem of rice and genes thereof				
JOURNAL	Patent: JP 2002315582-A 1 29-OCT-2002;				
COMMENT	NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES OS Oryza sativa L. cvs Nipponbare (rice) PN JP 2002315582-A/1 PD 29-OCT-2002 PF 24-APR-2001 JP 2001126682 PI KOICHI KADOWAKI,HIROAKI SHIMADA PC C12N15/09,A01H5/09,C07K14/415,C12N5/10,C12N5/00,C12N5/00 CC Novel proteins in phloem of rice and genes thereof FH Key Location/Qualifiers FT CDS (1)..(432).				
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Best Local Similarity	79.2%; Pred. No. 1.9e-65;				
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Db	1	ATGGTTCAGGGACGCTCGAGGTGCTCTCTCGTTCGAGCCCAAGGGCCCTCGAGAACCCGAC	60
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Qy	191	AGTATTGCAACTGGAAGGAAGTACCCCTGAGTGGGAATGAAAACCTTATCTCTCACTGTG	250
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Qy	251	TCTGACCGGACACAGACATTTGGTAATCAAGCTTATGGACAGTGTATCAGGCACAGACAGAT	310
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Qy	311	GACTTTGTTGGTGAAGCAAGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCA	370
Db	241	GATTTTGTGGGAAGCAACGATTTCTTTTGGGAAGCAATCTATCAGAAGGAGAGCTACCC	300
Qy	371	CCAACTCTTATATGTTGTGAAAGGTGAAAAATCTCGCGGGGAAATCAAAGTTGGTCTC	430
Db	301	CCAACTGTTTATATGTTGTGAAAGAGAGATACCGTGAGAGAAATCAAAGTTGGGCTG	360
Qy	431	ACATTCCTCTGAGGATATCTCGCAGCGGGGTCTCCAGAG---GACTTCGGTGGATGG	487
Db	361	ACGTTCACTCCAGAGGATGATCGCGATCGGGGTTTATCTGAGGAGACATTTGGTGGATGG	420
Qy	488	AAGCAATCATCT 499	
Db	421	AAGCAGTCATCT 432	
RESULT 5			
BT009547			
LOCUS	BT009547	874 bp	linear
DEFINITION	Triticum aestivum clone wr1.pk151.c12.f1s	874 bp	linear
ACCESSION	BT009547		PLN 20-JUN-2003
VERSION	BT009547.1		
KEYWORDS	FLI CDNA.		
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.		
AUTHORS	1 (bases 1 to 874) Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H., Caraher,N.R., Hanafey,M.K. and Hainey,C.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUN-2003) Crop Genetics, E. I. Dupont de Nemours and Company, 1 Innovation Way, P.O. Box 5104, Newark, DE 19714-6104, USA		
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Best Local Similarity	71.6%;	Pred. No. 5.1e-65;	
Matches 376;	Conservative	0; Mismatches 146;	Indels 3; Gaps 1
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Qy	94	GCTGCTCGTTGGGGCCAAAGGCGCTCGAGAACACCGATTACCTCTGTAAACATGATCCGTA	153
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Qy	154	TGCAATTCAGTGCCTGTTACAGAGACGAGACAGTATTGCAACTCGAAAGGAAC	213

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Oy 214 TACCCCTGAGTGAATGAACCTTTATCTTCACTGTGCTCAGCGGACACAGACTTGGT 273
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Oy 394 AGGTGAATAATCTCGGGGAAATCAAGATTTGGTCTCACATTTCACTCTCTGAGGATCTCG 453
Db 502 AGACGAAGATGACGTTGGAGAAATCAAAATTTGGTCTGACTCTCGGAGGAGCTCG 561
Oy 454 CCAGCGGGGTCTCCAGAGG---ACTTCGGTGGATGAAGCAATCATCTTAGAGCTAGAT 510
Db 562 TGATCAGGATCAACCCGAGGAACTATGTTGGTGGGGAACCAATCATCTTGAGAAGAC 621
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Db 622 AGTGTCTTGTGAACTATGTTGGTGCATGCTGCTAGTGA 666

RESULT 6
BV081654
LOCUS scl239_p3 Mol7 Zea mays Mol7 Zea mays STS 30-SEP-2003
DEFINITION site.
ACCESSION BV081654.1 GI:37053311
VERSION BV081654.1
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 72 81 75 77 74 81 79 68 65 63 57 59 54
54 55 56 57 67 62 62 52 62 82 88 82 76 64 63 59 72 86
86 86 81 76 68 61 62 54 72 59 58 55 62 54 61 72 78 61 61 57 67
56 70 61 63 63 71 40 40 28 28 28 45 51 45 45 63 63 79 69 78
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Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 514 TTAAGGGTGCACGAGCACAGCACAATTCATCGCTTGGAGCTTCAGCGCTCGAGTA 573
Db 1 TTAAGGGTGCACGAGCACAGCACAATTCATCGCTTGGAGCTTCAGCGCTCGAGTA 60
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Oy 694 TAAGCGCGTTGTGATTACTGCTTACACAGAGATTTGCTTCTAGTTCCTACCTACGCT 753
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Oy 754 TTTTITTT 760
Db 241 TTTTITTT 247

RESULT 7
BV081655
LOCUS scl239_p3 Ky21 Zea mays Ky21 Zea mays STS 30-SEP-2003
DEFINITION site.
ACCESSION BV081655
VERSION BV081655.1 GI:37053312
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM


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Db 241 TTTT TTTT 247

RESULT 9
BV109997
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DEFINITION
ACCESSION BV109997
VERSION BV109997.1 GI:45427618
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 247)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCTCTCTGAGGATCTCGC
Primer B: AGTATTACTGCTTACACCTCC
STS size: 247
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 35 46 42 42 39 35 39 34 30 30 32 32 58
49 49 47 51 53 65 70 62 78 56 57 56 65 62 82 81 81 75 72 61 64 59
61 68 71 71 63 68 64 57 56 73 61 64 52 62 51 59 66 60 70 65 73 55
40 37 37 30 30 30 51 51 40 45 55 66 66 72 72 71 71 62 59 59 77 69
76 76 71 66 66 82 88 85 86 86 84 80 77 69 69 64 63 63 66 82 88 90
90 89 82 82 80 69 70 65 65 60 68 86 90 72 69 70 61 60 63 68 73
67 69 68 72 60 64 64 76 73 90 78 84 76 76 85 90 90 90 88 81
74 73 80 80 80 80 80 82 89 87 83 74 71 71 71 76 73 80 80 89 89
77 80 74 80 74 68 50 50 56 56 56 44 44 44 43 43 42 73 66 70
74 83 74 71 74 78 79 76 75 67 61 59 64 70 43 43 42 42 43 40 31
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42 42 40 51 51 51 51 56 56 56 48 48 36.
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stages="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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STs
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ORIGIN

Query Match 28.2%; Score 247; DB 11; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.3e-57;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 513 TTTAAGGGTGCACAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGGTGCACAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCCGTCGAGT 60

OY 573 ACTTCATGCTTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGATTTGTTTCAGAGAAAGTG 632
Db 61 ACTTCATGCTTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGATTTGTTTCAGAGAAAGTG 120

OY 633 TTATTAGTAGTGTTCACAAAAATAGCTCCATATTCCTATATCCGTTATTCGAAATTT 692
Db 121 TTATTAGTAGTGTTCACAAAAATAGCTCCATATTCCTATATCCGTTATTCGAAATTT 180

OY 693 CTAAGGCCGTTTGTGATTACTGCTTACAACAAGAGTTTTCCTTCTAGTTCCCACTAGCG 752
Db 181 CTAAGGCCGTTTGTGATTACTGCTTACAACAAGAGTTTTCCTTCTAGTTCCCACTAGCG 240

OY 753 TTTT TTTT 759
Db 241 TTTT TTTT 247

RESULT 10
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LOCUS
DEFINITION scl239 p3 Kull1 Zea mays Kull1 Zea mays STS genomic, sequence tagged site.
ACCESSION BV081650
VERSION BV081650.1 GI:37053307
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 248)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)

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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCTCTCTGAGGATCTCGC
Primer B: AGTATTACTGCTTACACCTCC

PHRED/PHRAP Quality Scores 35 46 42 42 39 35 39 34 30 30 32 32 58
49 49 47 51 53 65 70 62 78 56 57 56 65 62 82 81 81 75 72 61 64 59
61 68 71 71 63 68 64 57 56 73 61 64 52 62 51 59 66 60 70 65 73 55
40 37 37 30 30 30 51 51 40 45 55 66 66 72 72 71 71 62 59 59 77 69
76 76 71 66 66 82 88 85 86 86 84 80 77 69 69 64 63 63 66 82 88 90
90 89 82 82 80 69 70 65 65 60 68 86 90 72 69 70 61 60 63 68 73
67 69 68 72 60 64 64 76 73 90 78 84 76 76 85 90 90 90 88 81
74 73 80 80 80 80 80 82 89 87 83 74 71 71 71 76 73 80 80 89 89
77 80 74 80 74 68 50 50 56 56 56 44 44 44 43 43 42 73 66 70
74 83 74 71 74 78 79 76 75 67 61 59 64 70 43 43 42 42 43 40 31
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42 42 40 51 51 51 51 56 56 56 48 48 36.

Location/Qualifiers
1..247
/organism="Zea mays"
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/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stages="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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STs

FEATURES

63 90 90 86 83	61 87 88 79 88	70 82 82 89 77	69 82 73 89 71	83 70 60 89 71	84 79 78 82 71	79 76 78 65 82	76 77 78 68 79	77 77 78 66 90	84 90 89 66 84	90 90 78 79 90	90 89 66 84 90	89 89 71 84 82
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Location/Qualifiers												
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/db_xref="taxon:4577"												
/clone_lib="Zea mays Kull1"												
/dev_stage="seedling"												
/note="Organ: leaf; genomic DNA from inbred line"												
<1..>248												

STS

ORIGIN

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Query Match      28.1%; Score 246.4; DB 11; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.9e-57;
Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   513 TTTAAGGGTGACACGAGCACAGCGACAATTCATGCCTTGGAGCCTTCAGCCGTTCGAGT 572
      |||||
Db    1 TTTAAGGGTGACACGAGCACAGCGACAATTCATGCCTTGGAGCCTTCAGCCGTTCGAGT 60
      |||||

Qy   573 ACTTCATGCTTAATCGAGAATTCATTGCAATTTGGCTTCTTTTGAATGTTTCAGAAAGTG 632
      |||||
Db    61 ACTTCATGCTTAATCGAGAATTCATTGCAATTTGGCTTCTTTTGAATGTTTCAGAAAGTG 120
      |||||

Qy   633 TTATTAGTAGTTTTCAACAAAAATAGCTCCATATTCCTCATATFCGGTATTCGTAATT 692
      |||||
Db    121 TTATTAGTAGTTTTCAACAAAAATAGCTCCATATTCCTCATATFCGGTATTCGTAATT 180
      |||||

Qy   693 CTAAGGCCGTTGTGATTACTGCTTACAAACAAGAGTTTTCGCTTCCCCTACGC 752
      |||||
Db    181 CTAAGGCCGTTGTGATTACTGCTTACAAACAAGAGTTTTCGCTTCCCCTACGC 240
      |||||

Qy   753 TTTTTTTT 760
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Db    241 TTTTTTTT 248
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RESULT 11
BV081657
LOCUS       BV081657                248 bp     DNA         linear     STS 30-SEP-2003
DEFINITION   sc1239 p3 Hp301 Zea mays Hp301 Zea mays STS genomic, sequence
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ACCESSION   BV081657
VERSION     BV081657.1 GI:37053314
KEYWORDS    STS.
SOURCE      Zea mays
            Zea mays
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 248)
AUTHORS     McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE       MPZ-UCI Joint SNP Discovery
JOURNAL     Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept.: Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACTCTCGAGGATACTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol: PCR amplification of genomic DNA
          Template: 50 ng
          Primer: each 0.5 uM
          dNTPs: each 200 uM

```

Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
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 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: ACATTCACCTCTGAGGATACATCGC
 Primer B: AGTATTACTGGCTACACCTCCC
 STS size: 248
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Tag Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 81 67 76 76 76 75 78 72 67 60 61 61 55
 55 52 57 58 56 62 65 52 61 58 65 62 76 65 71 73 84 78 77 71 67 82
 88 80 81 75 73 76 61 63 58 71 63 63 59 64 52 54 56 61 66 60 62 54
 59 58 66 55 55 74 79 75 66 57 57 82 87 90 89 90 65 37 40
 40 40 27 27 45 40 56 56 90 90 88 82 74 70 68 69 69 77 90 90
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 74 89 78 69 78 80 81 81 74 62 62 66 78 76 84 79 76 81 75 85
 85 73 69 63 67 69 75 77 56 56 56 55 55 55 56 56 56 56 56
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STS
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 Query Match 28.1%; Score 246.4; DB 11; Length 248;
 Best Local Similarity 99.6%; Pred. No. 4.9e-57;
 Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 513 TTTAAGGGTGACACGAGCAGACGACAAATTCATCGCTTGGAGCCTTCAGCCGTCGAGT 572
 1 TTTAAGGGTGACACGAGCAGACGACAAATTCATCGCTTGGAGCCTTCAGCCGTCGAGT 60
 Db 573 ACTTCATGCTAATGCAGAAATTCATTCGATTTGGCTTCTTTTGTATTTTTCAGAGAAGTG 632
 QY 61 ACTTCATGCTAATGAAGAATTCATTCGATTTGGCTTCTTTTGTATTTTTCAGAGAAGTG 120
 Db 633 TTATTAGTAGGTTTCAACAAAAATAGCTCCATATTCCTATATCCCGTATTGGAATTT 692
 Db 121 TTATTAGTAGGTTTCAACAAAAATAGCTCCATATTCCTATATTCCTGATTGGAATTT 180
 QY 693 CTAAGGCCGTTTGTGATTACTCTTACACAAAGAGTTTTCCTTCTAGTTCCTCCACTACGC 752
 Db 181 CTAAGGCCGTTTGTGATTACTCTTACACAAAGAGTTTTCCTTCTAGTTCCTCCACTACGC 240
 Y 753 TTTTITTTT 760

Query Match 28.1%; Score 246.4; DB 11; Length 248;
Best Local Similarity 99.6%; Pred. No. 4.9e-57;
Matches 247; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 513 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 572
DB 1 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 60

QY 573 ACTTCATGCTAATGCGAGAATTCATGATTTGGCTTCTTTTGAATTTTCAGAGAAGTG 632
DB 61 ACTTCATGCTAATGAGAATTCATGATTTGGCTTCTTTTGAATTTTCAGAGAAGTG 120

QY 633 TTATTAGTGAATTTCAACAAAAATAGCTCCATATTCCTATATCCCGTATTGGAAAT 692
DB 121 TTATTAGTGAATTTCAACAAAAATAGCTCCATATTCCTATATCCCGTATTGGAAAT 180

QY 693 CTAAGCCGTTTGTGATTTACTGCTTACAACAAGAGTTTGTCTTCTAGTTCCCACTACGC 752
DB 181 CTAAGCCGTTTGTGATTTACTGCTTACAACAAGAGTTTGTCTTCTAGTTCCCACTACGC 240

QY 753 TTTTITTTT 760
DB 241 TTTTITTTT 248

RESULT 14
BV081652
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BV081652 246 bp DNA linear STS 30-SEP-2003
sc1239_p3 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
site.

BV081652
BV081652.1 GI:37053309
STS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

Contact: Brandon S. Gaut
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U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primers: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 89 90 84 84 84 82 87 79 73 66 52 50 50
51 51 53 56 51 67 67 57 66 55 57 60 76 67 72 80 80 83 70 66 61 63

FEATURES
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ORIGIN

Query Match 28.1%; Score 246; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 572
DB 1 TTTAAGGGTGCCACGAGACAGCAGCAATTCATGCGCTTGAGCGCTTCAGCGCTCGAGT 60

QY 573 ACTTCATGCTAATGCGAGAATTCATTCGATTTGGCTTCTTTTGAATTTTCAGAGAAGTG 632
DB 61 ACTTCATGCTAATGCGAGAATTCATTCGATTTGGCTTCTTTTGAATTTTCAGAGAAGTG 120

QY 633 TTATTAGTGAATTTCAACAAAAATAGCTCCATATTCCTATATCCCGTATTGGAAAT 692
DB 121 TTATTAGTGAATTTCAACAAAAATAGCTCCATATTCCTATATCCCGTATTGGAAAT 180

QY 693 CTAAGCCGTTTGTGATTTACTGCTTACAACAAGAGTTTGTCTTCTAGTTCCCACTACGC 752
DB 181 CTAAGCCGTTTGTGATTTACTGCTTACAACAAGAGTTTGTCTTCTAGTTCCCACTACGC 240

QY 753 TTTTITTTT 758
DB 241 TTTTITTTT 246

RESULT 15
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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PZA01487 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
site.

BV109993
BV109993.1 GI:45427614
STS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ACATTCACCTCTGAGGATACCTCGC
Primer B: AGTATTACTGGCTACACCTCCCC
STS size: 246
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primers: each 0.5 uM
dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 89 90 84 84 84 82 87 79 73 66 52 50 50
51 51 53 56 51 67 67 57 66 55 57 60 76 67 72 80 80 83 70 66 61 63
70 64 84 70 66 72 56 56 63 71 76 71 77 63 65 65 81 83 69 64 55
40 35 39 24 24 46 46 37 37 29 29 40 43 40 39 22 22 22 35 43
46 51 72 61 61 77 80 86 79 85 90 85 82 72 70 65 65 65 66 88 90 90
90 87 87 85 85 79 73 61 56 56 72 79 79 69 63 65 58 54 54 61 69
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FEATURES
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Location/Qualifiers
/organism="Zea mays"
/molecule="genomic DNA"
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STS
ORIGIN

Query Match 28.1%; Score 246; DB 11; Length 246;
Best Local Similarity 100.0%; Pred. No. 6.3e-57;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 513 TTTAAGGGTGACACAGACAGACAGCAATTCATCGCGCTTGAGCCCTTCAGCCGTCGAGT 572
Db 1 TTTAAGGGTGACACAGACAGACAGCAATTCATCGCGCTTGAGCCCTTCAGCCGTCGAGT 60

Qy 573 ACTTCATGCTAATGCAGAAATTCATCGAAATTTGGCTTCTTTTGATTTTCAGAGAAGTG 632
Db 61 ACTTCATGCTAATGCAGAAATTCATCGAAATTTGGCTTCTTTTGATTTTCAGAGAAGTG 120

Qy 633 TTATTAGTGAGTTTCAACAAAAATAGCTCCATATTCCTCTATATCCGTATTCGAAAT 692
Db 121 TTATTAGTGAGTTTCAACAAAAATAGCTCCATATTCCTCTATATCCGTATTCGAAAT 180

Qy 693 CTAAGGCGGTTTGATTTACTGCTTACAAAGAAAGTTTTCCTTCTAGTCCCACTACGC 752
Db 181 CTAAGGCGGTTTGATTTACTGCTTACAAAGAAAGTTTTCCTTCTAGTCCCACTACGC 240

Qy 753 TTTTTT 758
Db 241 TTTTTT 246

Search completed: January 8, 2005, 10:24:44
Job time : 4018 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 04:44:49 ; Search time 526 Seconds
(without alignments)
8742.382 Million cell updates/sec

Title: US-09-913-569B-5

Perfect score: 876

Sequence: 1 gcacgaggttcgttcacgcc.....tttttgatccttgaaaaa 876

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	876	100.0	876	3 AAC79350	Aac79350 Plant vir
2	440	50.2	544	3 AAC79365	Aac79365 Plant vir
3	276.8	31.6	432	10 ADCS3921	Adcs3921 DNA encod
4	275.4	31.4	874	3 AAC79352	Aac79352 Plant vir
5	247.2	28.2	916	3 AAC79349	Aac79349 Plant vir
6	228	26.0	442	12 ADJ39772	Adj39772 Plant vir
7	226.2	25.8	683	8 AAD54388	Aad54388 Lolium pe
8	226.2	25.8	707	8 AAD54387	Aad54387 Lolium pe
9	226.2	25.8	828	8 AAD54386	Aad54386 Lolium pe
10	224.6	25.6	1110	8 AAD54408	Aad54408 Lolium pe
11	219	25.0	617	3 AAC79364	Aac79364 Plant vir
12	208.8	23.8	780	12 ADJ3944	Adj3944 Plant vir
13	194.8	22.2	770	3 AAC79361	Aac79361 Plant vir
14	191.8	21.9	615	6 ABQ66259	Abq66259 Arabidops
15	190.2	21.7	697	3 AAC36982	Aac36982 Arabidops
16	187.2	21.4	459	3 AAC79366	Aac79366 Plant vir
17	186.8	21.3	450	3 AAC79348	Aac79348 Plant vir
18	178.6	20.4	695	3 AAC79363	Aac79363 Plant vir
19	174.8	20.0	771	3 AAC79351	Aac79351 Plant vir
20	168.2	19.2	429	12 ADJ44911	Adj44911 Plant vir
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ALIGNMENTS

RESULT 1

AAC79350

ID AAC79350 standard; cDNA; 876 BP.

XX AC AAC79350;

XX DT 06-FEB-2001 (first entry)

XX DE Plant viral movement protein encoding cDNA SEQ ID 5.

XX KW Plant viral movement protein; transport; transgenic plant;

XX KM viral resistance; cosuppression; ss.

XX OS Zea mays.

XX PN WO200060088-A2.

XX PD 12-OCT-2000.

XX PF 06-APR-2000; 2000WO-US009110.

XX PR 07-APR-1999; 99US-0128092P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Krebbers E, Weng Z, Cahoon RE;

XX DR WPI; 2000-638467/61.

XX DR P-PSDB; AAB44496.

XX PT Novel viral movement polypeptides and polynucleotides useful in field of plant molecular biology, for producing transgenic plants, to prepare antibodies and in immunological screening of cDNA expression libraries.

XX PS Claim 2; Page 36; 62pp; English.

XX CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement proteins AAB4494-B44520. Some plant viruses have been shown to be able to establish systemic infections via movement proteins that utilize existing plant pathways to traffic macromolecules to surrounding cells. Proteins such as those of the invention are similar to viral movement proteins that function in the transport of nucleic acids from cell to cell. The plant viral movement proteins are useful for obtaining a nucleic acid fragment encoding a viral movement protein. Polynucleotides

Aac79375 Plant vir
Aac36910 Arabidops
Aac79373 Plant vir
Aac79139 Strawberry
Aac79374 Plant vir
Aac79357 Plant vir
Aac79358 Plant vir
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Aac79370 Plant vir
Aac79359 Plant vir
Aac79356 Plant vir
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Adq06646 Soybean t
Adc53925 DNA encod
Aac46286 Arabidops
Aac45546 Arabidops
Aac33283 Arabidops
Aac79371 Plant vir
Abz14738 Arabidops
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Abl74347 Corn tass
Adc53923 DNA encod
Aac79368 Plant vir

CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 876 BP; 241 A; 176 C; 226 G; 233 T; 0 U; 0 Other;

Query Match 100.0%; Score 876; DB 3; Length 876;
Best Local Similarity 100.0%; Pred. No. 6e-261;
Matches 876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACGAGGTTGCTTACGCCACAGGCAAGGCAAGGGCTTGTGAGGAGCGAGGAGC 60
DB 1 GCACGAGGTTGCTTACGCCACAGGCAAGGCAAGGGCTTGTGAGGAGCGAGGAGC 60
QY 61 GGAGGAGGACATGCTGTCACGGGACGCTGGAAGTCTGCTCGTTGGGGCCCAAGGGCTCGA 120
DB 61 GGAGGAGGACATGCTGTCACGGGACGCTGGAAGTCTGCTCGTTGGGGCCCAAGGGCTCGA 120
QY 121 GAACACCGATTACCTCTGTAACATGATCGGTATGCAATTCCTCAAGTGCCTTACAGGA 180
DB 121 GAACACCGATTACCTCTGTAACATGATCGGTATGCAATTCCTCAAGTGCCTTACAGGA 180
QY 181 GCAGAGAGCAGTATTGCAACTCGAAAGAACTACCCCTGAGTGGAAATGAAACCTTTAT 240
DB 181 GCAGAGAGCAGTATTGCAACTCGAAAGAACTACCCCTGAGTGGAAATGAAACCTTTAT 240
QY 241 CTTTCACTGTCTGACGGGACACAGACTTGGTAATCAAGCTTATGACAGTGATACAGG 300
DB 241 CTTTCACTGTCTGACGGGACACAGACTTGGTAATCAAGCTTATGACAGTGATACAGG 300
QY 301 CACAGCAGATGACTTGTGCTGCAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAG 360
DB 301 CACAGCAGATGACTTGTGCTGCAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAG 360
QY 361 GAGCATTTCACCAACTCTTATATGTTGGAAGGTGAAATATCTGCGGGGAAATCAA 420
DB 361 GAGCATTTCACCAACTCTTATATGTTGGAAGGTGAAATATCTGCGGGGAAATCAA 420
QY 421 AGTTGCTCTCATTCTACTCTGAGTACTCCAGCGGGGTCTCCAGAGACTTCGG 480
DB 421 AGTTGCTCTCATTCTACTCTGAGTACTCCAGCGGGGTCTCCAGAGACTTCGG 480
QY 481 TGGATGGAAGCAATCATCTTAGAGTAGATGCTTTTAAGGTGCACAGAGCAGCGACA 540
DB 481 TGGATGGAAGCAATCATCTTAGAGTAGATGCTTTTAAGGTGCACAGAGCAGCGACA 540
QY 541 ATTATGCGTTGGAGCCTTACGCGTCGAGTACTTCAATGCTTAATGAGAAATTCATTCA 600
DB 541 ATTATGCGTTGGAGCCTTACGCGTCGAGTACTTCAATGCTTAATGAGAAATTCATTCA 600
QY 601 TTTGGCTCTCTTATGTTTTCAGAAAGTGTATTAGTGTTCATCAACAAAATATAGC 660
DB 601 TTTGGCTCTCTTATGTTTTCAGAAAGTGTATTAGTGTTCATCAACAAAATATAGC 660
QY 661 TCCATATTGCTCTATATCCCGTATTGGAATTTCTTAAGCGCGTTTGTGATTACTGCTTACA 720
DB 661 TCCATATTGCTCTATATCCCGTATTGGAATTTCTTAAGCGCGTTTGTGATTACTGCTTACA 720
QY 721 ACAAGAAGTTTGTCTTCTAGTTCCTACCTACGCTTTTTTTTGAAGTTTGTAGTGGAAATC 780
DB 721 ACAAGAAGTTTGTCTTCTAGTTCCTACCTACGCTTTTTTTTGAAGTTTGTAGTGGAAATC 780
QY 781 TTTTGTGTTCAACGTTTGGGAGGTGTAGGCCAGTAACTACGAAAGAAATTAATTTCC 840
DB 781 TTTTGTGTTCAACGTTTGGGAGGTGTAGGCCAGTAACTACGAAAGAAATTAATTTCC 840
QY 841 CTTTGCAGCAACATTGTTTTTTTGTGATCCTTTGAAAAA 876

DB 841 CTTGCGACCAACATTGTTTTTTGTGATCCTTGAAAAA 876

RESULT 2
AAC79365
ID AAC79365 standard; cDNA; 544 BP.

XX AAC79365;

XX 06-FEB-2001 (first entry)

XX Plant viral movement protein encoding cDNA SEQ ID 35.

XX Plant viral movement protein; transport; transgenic plant;

XX Viral resistance; cosuppression; ss.

XX Zea mays.

XX WO200060088-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009110.

XX 07-APR-1999; 99US-0128092P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Krebbers E, Weng Z, Cahoon RE;

XX P-PSDB; AAB44511.

XX WPI; 2000-638467/61.

XX Novel viral movement polypeptides and polynucleotides useful in field of
XX plant molecular biology, for producing transgenic plants, to prepare
XX antibodies and in immunological screening of cDNA expression libraries.

XX Disclosure; Page 53; 62pp; English.

XX Polynucleotide sequences AAC79348-C79375 encode plant viral movement
XX proteins AAB4494-B44520. Some plant viruses have been shown to be able
XX to establish systemic infections via movement proteins that utilize
XX existing plant pathways to traffic macromolecules to surrounding cells.
XX Proteins such as those of the invention are similar to viral movement
XX proteins that function in the transport of nucleic acids from cell to
XX cell. The plant viral movement proteins are useful for obtaining a
XX nucleic acid fragment encoding a viral movement protein. Polynucleotides
XX encoding the plant viral movement proteins are useful for positive
XX selection of a transformed cell. The proteins are useful in the field of
XX plant molecular biology, and in the preparation of antibodies against the
XX proteins. The proteins are also useful for isolating cDNAs and genes
XX encoding homologous proteins from the same or other plant species, and to
XX create transgenic plants in which the protein is presented at higher or
XX lower levels than normal or in cell types or developmental stages in
XX which they are not normally found. The proteins and nucleotide sequences
XX may be used to control cosuppression and engineer plant virus resistance

XX Sequence 544 BP; 154 A; 120 C; 144 G; 118 T; 0 U; 8 Other;

Query Match 50.2%; Score 440; DB 3; Length 544;
Best Local Similarity 96.4%; Pred. No. 1.1e-125;
Matches 460; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 8 GTTCGTTACCGCCACAGGCAAGGCAAGGGCTTGTGAGGAGAGCGAGGAGCGAGGAG 67

DB 1 GTTCGTTACCGCCACAGGCAAGGCAAGGGCTTGTGAGGAGAGCGAGGAGCGAGGAG 60

QY 68 GACATGTTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGCGCTTCGAGAAACACC 127

DB 61 GACATGTTGCACGGGACGCTGGAAGTGTCTGTTGGGGCCCAAGGCGCTTCGAGAAACACC 120

QY 128 GATTACCTCTGTAACATGGATCCGATCGCAATTCCTCAAGTCCGTTTCACAGGAGCAGNAG 187

Db 121 GATTACCTCTGTAAACATGGATCCGATATGCAATTCCTCAAGTGCCGTTACAGGAGCAGAAG 180
Qy 188 AGCAGTATTGCAACTGGAAGAAAGAACTACCCCTCAGTGGAAATGAAACTTTATCTTCCT 247
Db 181 AGCAGTATTGCAACTGGAAGAAAGAACTACCCCTCAGTGGAAATGAAACTTTATCTTCCT 240
Qy 248 GTGCTCTGACCGGACACAGACTTGGTAAATCAAGCTTATGGACAGTATACAGGCACAGCA 307
Db 241 GTGCTCTGACCGGACACAGACTTGGTAAATCAAGCTTATGGACAGTATACAGGCACAGCA 300
Qy 308 GATGACTTTGTTGGTGAAGCAACGATTCCTCATTTGAAGCAGTGTATCTGAAAGAGCATT 367
Db 301 GATGACTTTGTTGGTGAAGCAACGATTCCTCATTTGAAGCAGTGTATCTGAAAGAGCATT 360
Qy 368 CCACCAACACTCTATAATGTTGTCGAAAGGTGAAATACTGCGGGGAAATCAAAAGTTGGT 427
Db 361 CCACCAACACTCTATAATGTTGTCGAAAGGTGAAATACTGCGGGGAAATCAAA-NTGGT 419
Qy 428 CTCACATTCACTCTGAGGATCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGGA 484
Db 420 CTCACATTCACTCTGAGGATCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGGA 476

RESULT 3

ADCS3921
ID ADCS3921 standard; DNA; 432 BP.
XX
AC ADCS3921;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA encoding rice phloem protein of the invention #1.
XX
KW Rice; ds; gene; phloem protein; Ca2+/phospholipid-combining domain;
KW promoter; transgenic plant; phloem-specific; exotic protein;
KW virus MP-like gene.
XX
OS Oryza sativa.

Key Location/Qualifiers

FT CDS 1..432
FT /product= "phloem protein #1"
FT /tag= a
FT /transl_except= (pos:61..63,aa:Trp)
FT /transl_except= (pos:82..84,aa:Trp)
FT /transl_except= (pos:280..282,aa:Trp)
FT /transl_except= (pos:310..312,aa:Trp)
FT /transl_except= (pos:334..336,aa:Trp)

PN JP2002315582-A.

XX

XX 29-OCT-2002.

PD

XX 24-APR-2001; 2001JP-00126682.

XX 24-APR-2001; 2001JP-00126682.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

PA WPI; 2003-407228/39.

XX P-PSDB; ADCS3922.

DR

XX A new protein in rice phloem and its gene, a DNA, a promoter, a

PT transgenic plant.

XX

XX Claim 8; SEQ ID NO 1; 18pp; Japanese.

XX

XX The invention discloses a rice phloem protein having Ca2+/phospholipid-

CC combining domain. Also claimed is a DNA encoding the novel rice phloem

CC protein, a promoter comprising a 1288 or 1572 base pair sequence, given

CC in the specification, a transgenic plant transformed to express phloem-

CC specifically the novel rice phloem protein, preparation of the novel rice

CC phloem protein by using the transgenic plant, a transgenic plant which
CC produces, phloem-specifically, an exotic protein. The method is used for
CC producing an exotic protein specifically in the phloem of a plant. The
CC gene represents a new virus MP-like gene from rice. The sequence
CC presented is a DNA encoding a rice phloem protein of the invention.
XX
SQ Sequence 432 BP; 122 A; 93 C; 124 G; 93 T; 0 U; 0 Other;

Query Match 31.6%; Score 276.8; DB 10; Length 432;
Best Local Similarity 79.2%; Pred. No. 4.8e-75;
Matches 342; Conservative 0; Mismatches 87; Indels 3; Gaps 1;

Qy 71 ATGTGTCACGGGACGTCGGAAGTCTCTCGTTGGGGCCAAAGGCCCTCGAGAACACCGAT 130
Db 1 ATGTGTCAGGGGACGTCGGAAGTCTCTCGTTGGGGCCAAAGGCCCTCGAGAACACCGAC 60
Qy 131 TACTCTGTAAACATGGATCCGATATGCAATTCCTCAAGTCCGCTTCACAGGAGCAGAGGC 190
Db 61 TACTCTGTAAACATGGATCCGATATGCAATTCCTCAAGTCCGCTTCACAGGAGCAGAGGC 120
Qy 191 AGTATTGCAACTCGGAAAGGAACCTACCCCTGAGTGGAAATGAAAACCTTTATCTTCAC 250
Db 121 AGGTTGCGTCAGGTAAGGATCTGACCCCTGAATGGAAACGAAACCTTTATGTTGTCAG 180
Qy 251 TCTGACCGGACAAACAGACTTTGGTAAATCAAGCTTATGGACAGTATACAGGCACAGCAG 310
Db 181 ACTCACAACGCTACAGAGCTCATCATCAAGTTGATGGACAGTGCACGTCGACCGATGAT 240
Qy 311 GACTTTGTTGGTGAAGCAACGATTCCTCATTTGAAGCAGTGTATCTGAAAGGAGCATTCCA 370
Db 241 GATTTTGTGGAGAACCAACGATTTCTTTTGGAAAGCAATCTATACAGAAAGCAATACCC 300
Qy 371 CCAACACTCTATAATGTTGTAAGGTAAGAAATCTCGCGGGAAATCAAAAGTTGGTCTC 430
Db 301 CCAACTGTTTATAATGTTGTAAGGTAAGAAATCTCGCGGGAAATCAAAAGTTGGTCTC 360
Qy 431 ACATTCACTCTCAGGATATCTCGCCAGCGGGGTCTCCAGAG---GACTTCGGTGGATGG 487
Db 361 ACGTTCACTCCAGAGGATGATCGGATCGGGGTTTATCTGAGGAAGACATTGGTGGATGG 420
Qy 488 AAGCAATCATCT 499
Db 421 AAGCAGTCATCT 432

RESULT 4

AAC79352

ID AAC79352 standard; cDNA; 874 BP.

XX

AC AAC79352;

XX

DT 06-FEB-2001 (first entry)

XX

XX Plant viral movement protein encoding cDNA SEQ ID 9.

XX Plant viral movement protein; transport; transgenic plant;

XX viral resistance; cosuppression; ss.

XX Triticum aestivum.

XX WO2000060088-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US0009110.

XX 07-APR-1999; 99US-0128092P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Kriebbers E, Weng Z, Cahoon RE;

XX WPI; 2000-638467/61.

XX

DR P-PSDB; AAB44498.
 XX Novel viral movement polypeptides and polynucleotides useful in field of
 PT plant molecular biology, for producing transgenic plants, to prepare
 PT antibodies and in immunological screening of cDNA expression libraries.
 XX
 PS Claim 2; Page 38; 62pp; English.
 XX
 CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
 CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
 CC to establish systemic infections via movement proteins that utilize
 CC existing plant pathways to traffic macromolecules to surrounding cells.
 CC Proteins such as those of the invention are similar to viral movement
 CC proteins that function in the transport of nucleic acids from cell to
 CC cell. The plant viral movement proteins are useful for obtaining a
 CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
 CC encoding the plant viral movement proteins are useful for positive
 CC selection of a transformed cell. The proteins are useful in the field of
 CC plant molecular biology, and in the preparation of antibodies against the
 CC proteins. The proteins are also useful for isolating cDNAs and genes
 CC encoding homologous proteins from the same or other plant species, and to
 CC create transgenic plants in which the protein is presented at higher or
 CC lower levels than normal or in cell types or developmental stages in
 CC which they are not normally found. The proteins and nucleotide sequences
 CC may be used to control cosuppression and engineer plant virus resistance
 XX
 SQ Sequence 874 BP; 261 A; 188 C; 223 G; 202 T; 0 U; 0 Other;

Query Match 31.4%; Score 275.4; DB 3; Length 874;
 Best Local Similarity 71.6%; Pred. No. 1.9e-74;
 Matches 376; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
 QY 34 AGGGCTTGTGAGGAGAGCGAGAGCGGAGGAGCATGGTGCACGGGACGCTGGAAGT 93
 DB 142 AGCGGAGAGGAGGCGAGATCAGCGCGGAGAGAGATGGCGAGGGGACGCTGGAGT 201
 QY 94 GCTCTCTGTTGGGCGGAGGCTTCGAGACACCGATTACTCTGTAAACATGATCCGTA 153
 DB 202 GCTCTCTGTTGGGCGGAGGCTTCGAGACACCGATTACTCTGTAAACATGATCCGTA 261
 QY 154 TGCAATCTCAAGTGGCGGTTTACAGGAGCAGAGAGCAGTATTGCACTGGAAAGGAAC 213
 DB 262 CGCGTCTTAAATGCACCTCGCAGGAGCAAAAGAGCACCGTCTCGTGGAAAGGAAG 321
 QY 214 TACCCCTGAGTGAATGAATACTTTATCTTCACTGTGTCTGACCGGACACACACTTGT 273
 DB 322 TGATCTCTGAGTGAACGAACCTTTGTGTTTACCGCTCTCTGAGAAATGCAACTGAGTGT 381
 QY 274 AATCAAGCTTATGACAGTGTATACAGGACAGCAGATGACTTTGTTGTTGAAGCAACGAT 333
 DB 382 CATCAAGCTTATGACAGTGTATGTTGCAACGAGCAGCAGCGTTGTTGAGACGAT 441
 QY 334 TCCATTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCAACCTCTATATGTTGAA 393
 DB 442 CCCATTGATGAGTGTACACTGAAGGAAGCATCCCACTGTTTACAAATGTTGCA 501
 QY 394 AGTGAAAAAATCTCGGGGAAATCAAGTTGGTCTCACATCTACTCTGAGGATCTCG 453
 DB 502 AGACGAAGAGTACCGTGAGAAATCAAAATTTGGTCTGACGTTCTACTCCGGAGGAGCTCG 561
 QY 454 CCAGCGGGGTCTCCAGAGG---ACTTCGGTGGATGGAAGCAATCATCTTAGAGCTAGAT 510
 DB 562 TGATCAGATCAACCCGAGGAACATATGTTGGTGGAAACCAATCATCTTGAGAAGAAGC 621
 QY 511 GCTTTAAGGTGCACACGAGCAGCAGCAATTCATGCGCTTGA 555
 DB 622 AGGTCTTGTGAACTATGGTGGCTGACAAAGTCGTGTGCTAGAA 666

RESULT 5
 AAC79349
 ID AAC79349 standard; cDNA; 916 BP.
 XX

AC AAC79349;
 XX
 DT 06-FEB-2001 (first entry)
 XX
 DE Plant viral movement protein encoding cDNA SEQ ID 3.
 XX
 KW Plant viral movement protein; transport; transgenic plant;
 KW viral resistance; cosuppression; ss.
 XX
 OS Zea mays.
 OS WO200060088-A2.
 PN 12-OCT-2000.
 XX
 PD 06-APR-2000; 2000WO-US009110.
 PF 07-APR-1999; 99US-0128092P.
 XX
 PR (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PA Krebbers E, Weng Z, Cahoon RE;
 PI WPI; 2000-638467/61.
 XX
 DR P-PSDB; AAB44495.
 DR
 XX Novel viral movement polypeptides and polynucleotides useful in field of
 PT plant molecular biology, for producing transgenic plants, to prepare
 PT antibodies and in immunological screening of cDNA expression libraries.
 XX
 PS Claim 2; Page 35; 62pp; English.
 XX
 CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
 CC proteins AAB44494-B44520. Some plant viruses have been shown to be able
 CC to establish systemic infections via movement proteins that utilize
 CC existing plant pathways to traffic macromolecules to surrounding cells.
 CC Proteins such as those of the invention are similar to viral movement
 CC proteins that function in the transport of nucleic acids from cell to
 CC cell. The plant viral movement proteins are useful for obtaining a
 CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
 CC encoding the plant viral movement proteins are useful for positive
 CC selection of a transformed cell. The proteins are useful in the field of
 CC plant molecular biology, and in the preparation of antibodies against the
 CC proteins. The proteins are also useful for isolating cDNAs and genes
 CC encoding homologous proteins from the same or other plant species, and to
 CC create transgenic plants in which the protein is presented at higher or
 CC lower levels than normal or in cell types or developmental stages in
 CC which they are not normally found. The proteins and nucleotide sequences
 CC may be used to control cosuppression and engineer plant virus resistance
 XX
 SQ Sequence 916 BP; 236 A; 231 C; 252 G; 197 T; 0 U; 0 Other;
 XX
 QY Query Match 28.2%; Score 247.2; DB 3; Length 916;
 Best Local Similarity 76.5%; Pred. No. 1.1e-65;
 Matches 303; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
 QY 52 GCGAGAGCGGAGGAGGACATGGTGCACGGGACGCTGGAGGTGCTGCTGGGGCCAA 111
 DB 215 GCTAACCCGCGGAGGAGAGATGGCGAGGGGACGCTGGAGGTGCTTCTCGTGGAGCCAG 274
 QY 112 GGGCTCTGAGAACACCGATTACTCTGTAAACATGGATCCGATGCAATTTCTCAAGTCCG 171
 DB 275 GGGCTCTGAGAACACCGATTACTCTGAGCAACATGGACCCCTACGCGCTTCTGCAATGTCG 334
 QY 172 TTCACAGGAGCAGAGAGCAGTATTGCAACTGGAAAGGAACCTACCCCTGAGTGGGAATGA 231
 DB 335 CTCCCACAGGAGCAGAGAGCAGCGTGCATCTGCAAAAGGCTGTGAACCTGAGTGGAAACGA 394
 QY 232 AAACTTTATCTTCACTGTGTCTGACCGGACACACAGACTTGGTAATCAAGCTTATGACAG 291
 DB 395 GACCTTCTGTTTCACTGTGTCTGATGGCGCAGCAGAGCTGTTTCATCAAGCTCTCTGACAG 454
 QY 292 TGATACAGGACAGCAGATGACTTTGTTGTTGAAGCAACGATTTCCATTGGAAGCAGTGA 351

DB 455 TGACGGTGGCACTGATGACGATTTTGTGGTGGCAACGATTCCTCTGGAAAGCAGTTTA 514
QY 352 TACTGAAAGGAGCATTCCACCAACACTCTATAATCTTGTGAAAGTGAAAAATACTGCGG 411
DB 515 CACGGNAGAAACATCCCTCGACTGTTTACATGTTTGTGAAGCAGGAAGTAATCCGCGG 574
QY 412 GGAATCAAAAGTTGTTCTCACATTCACCTCCTGAGGA 447
DB 575 AGAAATCAAAGTTGGCCTCAGCTTCACTCCAGAGGA 610

RESULT 6

ADJ39772
ID ADJ39772 standard; cDNA; 442 BP.

XX AC ADJ39772;

XX DT 06-MAY-2004 (first entry)

XX DE Plant cDNA #772.

XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX antifungal.

XX OS Eukaryota.

XX FN US2004016025-A1.

XX PD 22-JAN-2004.

XX PF 26-SEP-2002; 2002US-00260238.

XX PR 26-SEP-2001; 2001US-0325277P.

XX PR 04-APR-2002; 2002US-0370620P.

XX PA (BUDW/) BUDWORTH P.

XX PA (MOUG/) MOUGHAMER T.

XX PA (BRIG/) BRIGGS S P.

XX PA (COOP/) COOPER B.

XX PA (GLAZ/) GLAZEBROOK J.

XX PA (GOFF/) GOFF S A.

XX PA (KATA/) KATAGIRI F.

XX PA (KREP/) KREPS J.

XX PA (PROV/) PROVART N.

XX PA (RICK/) RICHE D.

XX PA (ZHUT/) ZHU T.

XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;

XX XX WPI; 2004-190374/18.

XX DR New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.

XX PS Claim 71; SEQ ID NO 772; 230pp; English.

XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 442 BP; 125 A; 97 C; 111 G; 109 T; 0 U; 0 Other;

Query Match 26.0%; Score 228; DB 12; Length 442;

Best Local Similarity 78.6%; Pred. No. 6.9e-60;

Matches 330; Conservative 0; Mismatches 45; Indels 45; Gaps 3;

QY 71 ATGGTGACGGGACGCTGGAAGTCTGCTGTGGGGCCAAAGGCCCTCGAGAACACCGAT 130

DB 1 ATGGTGACGGGACGCTGGAAGTCTGCTGTGGGGCCAAAGGCCCTCGAGAACACCGAT 60

QY 131 TACTCTCTGT-----AACATGGA 147

DB 61 TACTCTGTGTACGCATCAGCTTATAATCTTAAAGCGCATTTGCTTGAACATGGA 120

QY 148 TCCGTATGCAATCTCAAGTGCCGTTCCACAGGACAGAGCAGTATTGCAAC-TGGAA 206

DB 121 TCATATGCAATCTCAAGTGCCGTTCCACAGGACAGAGCAGTATTGCAAC-TGGAA 180

QY 207 AAGGAACCTCCCTGAGTGAATGAAATTTTCTTCTGCTGTGACCGGCAACAG 266

DB 181 AAGGAAGTAAACCTGATGGAACGAAATTTTCTTCTGCTGTGACCGGCAACAG 240

QY 267 ACTTGTGTAATCAAGCTTATGACAGTATACAGCAGCAGCAGTACTTGTGTTGTTGAG 326

DB 241 AGCTGTTGATCAAGCTCTTGGACAGTGTATCTGAAAGGAGCATTCCACCAACACTCTATAATG 300

QY 327 CAACGATTCCATTGGAAGCAGTGTATCTGAAAGGAGCATTCCACCAACACTCTATAATG 386

DB 301 CAAC-ATTCCTTTGGAAGCAGTGTATCTGAAAGGAGTATTCACCAACACTCTGTATAATG 359

QY 387 TTGTGAAAGTGAAAAATCTGCGGGGAAATCAAAGTTGGTCTCACAATTCCTCTGAGG 446

DB 360 TTGTGAAAGTGAAATCTGCTGTGGAGAAATCAAAGTCCGCTCACATTCACTCCTGAGG 419

RESULT 7

AAD54388

ID AAD54388 standard; DNA; 683 BP.

XX AC AAD54388;

XX DT 17-JUN-2003 (first entry)

XX DE Lolium perenne elicitor-responsive protein a2 (LpERA2) DNA.

XX KW Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DEF; ER;
XX KW elicitor-responsive protein; disease resistance; plant defence response;
XX KW protein storage; pest resistance; genetic marker; gene therapy; antipept;
XX KW agricultural; LpERA2; ds.

XX OS Lolium perenne.

XX PN WO20028359-A1.

XX PD 07-NOV-2002.

XX PF 01-MAY-2002; 2002WO-AU000539.

XX PR 02-MAY-2001; 2001AU-00004735.

XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX PA (AGRE-) AGRSEARCH LTD.


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Db      522 GGTGAGACAA 532
RESULT 9
AAD54386
ID      AAD54386 standard; DNA; 828 BP.
XX
AC      AAD54386;
XX
DT      17-JUN-2003 (first entry)
XX
DE      Lolium perenne elicitor-responsive protein a (LpEra) DNA.
XX
KW      Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DBF; ER;
KW      elicitor-responsive protein; disease resistance; plant defence response;
KW      protein storage; pest resistance; genetic marker; gene therapy; antipept;
KW      agricultural; LpEra; gene; ds.
XX
XX      Lolium perenne.
XX
FH      Key      Location/Qualifiers
FT      CDS      228..665
FT      /*tag= a
FT      /product= "Ryegrass Era (LpEra) protein"
XX
FN      WO200288359-A1.
XX
XX      07-NOV-2002.
XX
XX      01-MAY-2002; 2002WO-AU000539.
XX
XX      02-MAY-2001; 2001AU-00004735.
XX
XX      (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX      (AGRE-) AGRESEARCH LTD.
XX
XX      Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX      WPI; 2003-201227/19.
XX      P-PSDB; AAE35936.
XX
XX      New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like,
XX      elicitor-responsive or defensin polypeptide, for modifying disease and/or
XX      plant resistance, plant defence response and/or protein storage in a
XX      plant.
XX
XX      Claim 5; Fig 16; 195pp; English.
XX
XX      The invention relates to novel ryegrass (Lolium) or fescue (Festuca)
XX      nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-
XX      responsive (ER) or defensin (DEF) proteins and polynucleotides encoding
XX      such proteins. Sequences of the invention are useful to modify disease
XX      and/or pest resistance, plant defence response and/or protein storage in
XX      plants. The nucleotide sequence information and/or single nucleotide
XX      polymorphisms of the nucleic acid are useful as genetic markers. They are
XX      also useful in gene therapy. The present sequence is ryegrass Era (LpEra)
XX      DNA
XX
XX      Sequence 828 BP; 214 A; 199 C; 203 G; 198 T; 0 U; 14 Other;
XX
Query Match      25.8%; Score 226.2; DB 8; Length 828;
Best Local Similarity 70.3%; Pred. No. 3.5e-59;
Matches 303; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY      63 AGAGGACATGTGTCACGGACGCTGGAAGTGTCTGCTGGGGCCCAAGGGCTCGAGA 122
Db      223 AGAAGATGGCGCAGGCGCGGACGCTCGAGGTGTCTGCTCGGAGCCCAAGGGCTCGAGA 282
QY      123 ACACCGATTACCTCTGTAAACATGATCCGTATGCAATTCCTCAAGTGCCTTCACAGGAC 182
Db      283 ACACCGACTACCTGTGCAACATGATCCCTACGGCTTCTCAGAGTCACCTCAATGAGC 342
QY      183 AGAAGACAGTATTGCAACTGGAAAGGAACCTACCCCTGAGTGGATGAAAGAACTTTATCT 242

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Db      343 AGAGGAGCTCGTTTCAGAAAGGCAAGAGTGAAGCCGGAATGGAACGAAACCTTTGTGT 402
QY      243 TCACTGTGTCTGACCGGACACAGACTTGGTAATCAAGCTTATGGACAGTATACAGCA 302
Db      403 TCAGACCTCCGAAAACGCAACCGAGCTCTGCAATCAAGCTCCTGGACGACCAATGAA 462
QY      303 CAGCAGATGACTTTTGGTGAAGCAACGATTTCCATTGGAAAGCAGTGTATATCTGAAAGGA 362
Db      463 CCAACGACGACGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTCTATCTAGAGAA 522
QY      363 GCATTCCACCAACTCTTATAATTTGTGAAAGTGAAATACTCGGGGAAATCAAG 422
Db      523 GCATACCACCAACAGTTTACAATTTGTCAAAGATGAAGAGTACTGTGGAGAAATCAGAA 582
QY      423 TTGTCTCACATTCACCTCTGAGGATACTCGCCAGCGGGTCTCCAGAGGACATTCGGTG 482
Db      583 TTGTCTCAAGTTTCACTCCGAGGAGGCTTACCATTATTACCCGAGGAAAACTTCGGTG 642
QY      483 GATGGAAGCAA 493
Db      643 GGTGAGACAA 653

```

RESULT 10

AAD54408

ID AAD54408 standard; cDNA; 1110 BP.

XX AAD54408;

AC AAD54408;

XX 17-JUN-2003 (first entry)

XX Lolium perenne elicitor-responsive protein a (LpEra) cDNA.

XX Ryegrass; thionin; TH; thaumatin-like protein; TL; defensin; DBF; ER;

XX elicitor-responsive protein; disease resistance; plant defence response;

XX protein storage; pest resistance; genetic marker; gene therapy; antipept;

XX agricultural; LpEra; gene; ss.

XX Lolium perenne.

XX Key Location/Qualifiers

FH CDS 326..712

FT /*tag= a

FT /product= "Ryegrass Era (LpEra) protein"

XX WO200288359-A1.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-AU000539.

XX 02-MAY-2001; 2001AU-00004735.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX (AGRE-) AGRESEARCH LTD.

XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;

XX WPI; 2003-201227/19.

XX P-PSDB; AAE35945.

XX New ryegrass or fescue nucleic acid encoding a thionin, thaumatin-like, or

XX elicitor-responsive or defensin polypeptide, for modifying disease and/or

XX plant resistance, plant defence response and/or protein storage in a

XX plant.

XX Claim 5; Fig 49; 195pp; English.

XX The invention relates to novel ryegrass (Lolium) or fescue (Festuca)

XX nucleic acids encoding thionin (TH), thaumatin-like (TL), elicitor-

XX responsive (ER) or defensin (DEF) proteins and polynucleotides encoding

XX such proteins. Sequences of the invention are useful to modify disease

CC and/or pest resistance, plant defence response and/or protein storage in
CC plants. The nucleotide sequence information and/or single nucleotide
CC polymorphisms of the nucleic acid are useful as genetic markers. They are
CC also useful in gene therapy. The present sequence is ryegrass Era (UpEra)
CC cDNA
XX
SQ Sequence 1110 BP; 322 A; 258 C; 275 G; 255 T; 0 U; 0 Other;

Query Match 25.6%; Score 224.6; DB 8; Length 1110;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 302; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 63 AGGAGGACATGTTGTCACGGAGCGCTGGAAGTGTCTGCTGTGGGCGCAAGGCGCTCGAGA 122
Db 321 AGAAGATGGCGGCGGCGGAGCGCTCGAGTGTCTGCTGTGGAGCCAAAGGGGCTCGAGA 380
QY 123 ACACCGATTACCTCTCTTAACATGATCCGCTATGCAATTTCTCAAGTGCCTTTCACAGGAGC 182
Db 381 ACACCGACTACCTGTGCAACATGATCCCTAGCGCTTCTCAGAGTCACCTCCAAATGAGC 440
QY 183 AGAAGAGCAGTATTGCAACTGGAAGAACTACCCCTGAGTGGATGAAATCTTATCT 242
Db 441 AGAGGAGCTCCGTTGCGAAGGCAAGGAAGTGAAGCGGGAATGGAACGAACCTTTGTGT 500
QY 243 TCACTGTGTGACCGGACACAGACTTGTATCAAGCTTATGGACAGTGTATACAGGCA 302
Db 501 TCAGGACTTCGAAACGACCGAGCTCTGCATCAAGCTCTGGACGACGCAATGGAA 560
QY 303 CAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTGGAAGCAGTGTATCTGAAAGGA 362
Db 561 CCAACGACGAGGATGTTGGTGAAGCAAGGATCCCTCTGGATGCTGTCTATATGAAGAA 620
QY 363 GCATTCACCAACACTCTATATGTTGTGAAGGTGAAATACTCCGGGGAAATCAAG 422
Db 621 GCATACCAACCAAGTTTACATGTTGTCAAAGATGAAGAGTACTGTGGAGAAATCAGAA 680
QY 423 TTGGTCTCAGATTCACCTCTGAGGATACCTCGCCAGCGGGTCTCCAGAGGACTTCGGTG 482
Db 681 TTGGTCTCAAGTTCACTTCGGAGGAGCTTAGCATTTATTACCCGAGGAAATCTCGGTG 740
QY 483 GATGGAAGCA 493
Db 741 GGTGGAGACAA 751

RESULT 11
AAC79364
ID AAC79364 standard; cDNA; 617 BP.
XX AAC79364;
XX
XX
DT 06-FEB-2001 (first entry)
XX
XX Plant viral movement protein encoding cDNA SEQ ID 33.
DE
XX Plant viral movement protein; transport; transgenic plant;
KW viral resistance; cosuppression; ss.
XX
XX Zea mays.
XX
XX WO200060088-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009110.
XX
XX 07-APR-1999; 99US-0128092P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Krebbers E, Weng Z, Cahoon RE;
XX
XX WPI; 2000-638467/61.
DR

DR P-PSDB; AAB44510.
XX
XX Novel viral movement polypeptides and polynucleotides useful in field of
PT plant molecular biology, for producing transgenic plants, to prepare
PT antibodies and in immunological screening of cDNA expression libraries.
XX
XX Disclosure; Page 51; 62pp; English.

XX
CC Polynucleotide sequences AAC79348-C79375 encode plant viral movement
CC proteins AAB4494-B44520. Some plant viruses have been shown to be able
CC to establish systemic infections via movement proteins that utilize
CC existing plant pathways to traffic macromolecules to surrounding cells.
CC proteins such as those of the invention are similar to viral movement
CC proteins that function in the transport of nucleic acids from cell to
CC cell. The plant viral movement proteins are useful for obtaining a
CC nucleic acid fragment encoding a viral movement protein. Polynucleotides
CC encoding the plant viral movement proteins are useful for positive
CC selection of a transformed cell. The proteins are useful in the field of
CC plant molecular biology, and in the preparation of antibodies against the
CC proteins. The proteins are also useful for isolating cDNAs and genes
CC encoding homologous proteins from the same or other plant species, and to
CC create transgenic plants in which the protein is presented at higher or
CC lower levels than normal or in cell types or developmental stages in
CC which they are not normally found. The proteins and nucleotide sequences
CC may be used to control cosuppression and engineer plant virus resistance
XX
SQ Sequence 617 BP; 147 A; 160 C; 176 G; 133 T; 0 U; 1 Other;

Query Match 25.0%; Score 219; DB 3; Length 617;
Best Local Similarity 75.1%; Pred. No. 5.2e-57;
Matches 299; Conservative 0; Mismatches 96; Indels 3; Gaps 2;
QY 52 GCGAGGACGCGGAGGAGACATGCTCAGCGGACGCTGGAAGTGTCTGCTGGGCGCAA 111
Db 208 GCCAACCCGCGGAGGAGAGATGGCGCAGGGGACGCTGGAGGTGCTTCTGTCGAGGCCAG 267
QY 112 GGGCTCTCAGAACACCGGATTACCTCTGTAACATGATCCGTATGCAATTTCTCAAGTGCCG 171
Db 268 GGGCTCTCAGAACACCGGATTACCTGAGCAACATGACCCCTACGGCTTCTGCAATGTGCG 327
QY 172 TTCACAGGAGCAGAGAGCAGTATTGGCACTGGAAAGGAACTACCCCTGAGTGAATGA 231
Db 328 CTCACACGAGCAGAGAGCAGCGTGCATCTGGCAAGGCTGTGAACCTGAGTGAACGA 387
QY 232 AAACCTTTATCTCAGTGTCTGACCGGACACACACTGGTAATCAAGCTTATGACAG 291
Db 388 GACCTTCGTGTTACCGTCTCCACGGCGCACANGAGCTGTTTCATCAAGCTCTCGACAG 447
QY 292 TGATACAGCAGCAGAGATGACTTTTGGTGAAGCAACGATTCCATTGGAAG-CAGTGT 350
Db 448 TGACCGTGGCACTGATGACGATTTTGGTGAAGCAACGATTCTCTGGAAGCCAGTTT 507
QY 351 ATACTGAAAGGA--GCATTTCACCAACACTCTATATGTTGGAAGGTGAAATACTG 408
Db 508 ACACGGGAAGGAAGCATTCCTTCCGACTGTTTACAAATGTTGTAAGACGAAGATACCG 567
QY 409 CGGGAAATCAAGTTGTTCTCAGATTCTCCTCTGAGG 446
Db 568 CGGAGAAATCAAGTTGGCTCAGCTTCACTCCAGAGG 605

RESULT 12
ADJ43944/c
ID ADJ43944 standard; cDNA; 780 BP.
XX
XX ADJ43944;
XX
XX 06-MAY-2004 (first entry)
XX
XX Plant cDNA #4944.
DE
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW

Qy	471	AGGACTTCGGTGGATGCAACCAATCATCTTA	501
Db	183	AGGAGTCTATGGGGCTGGAAAACTCTGA	153
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ID	AAC36982	standard; DNA; 697 BP.	
XX	AC	AAC36982;	
DT	17-OCT-2000	(first entry)	
XX	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 15760.	
DE	XX	Hybridisation assay; genetic mapping; gene expression control;	
KW	KW	protein identification; signal transduction pathway; metabolic pathway;	
KW	KW	promoter; termination sequence; ss.	
XX	XX	Arabidopsis thaliana.	
OS	XX	EP1033405-A2.	
PN	PN	06-SEP-2000.	
XX	XX	25-FEB-2000; 2000EP-00301439.	
PF	PF	99US-0121825P.	
XX	XX	99US-01231825P.	
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PR	PR	23-MAR-1999; 99US-0125788P.	
PR	PR	25-MAR-1999; 99US-0126264P.	
PR	PR	29-MAR-1999; 99US-0126785P.	
PR	PR	01-APR-1999; 99US-0127462P.	
PR	PR	06-APR-1999; 99US-0128234P.	
PR	PR	08-APR-1999; 99US-0128714P.	
PR	PR	16-APR-1999; 99US-0129845P.	
PR	PR	19-APR-1999; 99US-0130077P.	
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Db	139	AAGGTCTCGAGGACGAGATTTTCTGAAATAACATGGATCCTTATGTGCAACTCACTTGT	198		

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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	37.2	4.2	2958	4	US-09-688-078-5
C 4	37	4.2	2465	4	US-09-205-258-206
5	36	4.1	2229	4	US-09-799-451-554
6	36	4.1	5917	4	US-09-780-175-17
C 7	35.4	4.0	1141	4	US-09-806-708B-22
8	35.2	4.0	801	4	US-09-252-991A-4545
C 9	35.2	4.0	969	4	US-09-252-991A-4308
10	35.2	4.0	1284	4	US-09-286-981B-24
C 11	34.2	3.9	507	4	US-09-513-999C-10484
12	34.2	3.9	1548	4	US-09-248-796A-6167
C 13	33.8	3.9	710	3	US-09-988-416-256
14	33.8	3.9	11050	4	US-10-204-708-86
C 15	33.8	3.9	392000	4	US-10-027-983-11
C 16	33.6	3.8	575	4	US-09-513-999C-10483
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21	33.6	3.8	1360	4	US-09-536-784-37
22	33.6	3.8	4149	2	US-08-737-715-1
23	33.6	3.8	4723	4	US-09-023-655-1137
24	33.6	3.8	12665	4	US-08-961-527-134
C 25	33	3.8	580073	4	US-08-545-528D-1
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27	32.8	3.7	837	4	US-09-270-767-18916

28	32.8	3.7	1245	4	US-09-774-528-372	Sequence 372, Appl
29	32.6	3.7	319608	4	US-09-539-333D-1	Sequence 1, Appl
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32	32.6	3.7	250	3	US-09-568-315-16	Sequence 16, Appl
33	32.6	3.7	366	4	US-09-513-999C-8827	Sequence 8827, Ap
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39	32.4	3.7	1148	4	US-09-665-189A-75	Sequence 75, Appl
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ALIGNMENTS

RESULT 1
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; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-F15
; US-08-232-463-14
Query Match 5.1%; Score 44.6; DB 1; Length 7218;

Best Local Similarity 2.2%; Pred. No. 0.00082;
Matches 8; Conservative 207; Mismatches 146; Indels 0; Gaps 0;

QY 3 ACAGAGTTCGTTACGCCACAGCAAGGACAGGGGCTTGTGAGGAGAGCGAGGCGG 62
Db 1447 AAGAAATTGGTACRR 1388
QY 63 AGAGGACATGGTGCACGGGACGCTGGAAGTGTCTGCTGGGGCGCAAGGGCTCGAGA 122
Db 1387 RRR 1328
QY 123 ACACGATTAACCTCTGTAACATGATCGGTATGCAATCTCAAGTCCGCTTCACAGGAGC 182
Db 1327 RRR 1268
QY 183 AGAAGACAGTATTGCAACTGGAAAGAACTACCCCTGAGTGAATGAAACTTTATCT 242
Db 1267 RRR 1208
QY 243 TCACTGTGTCTGACCGGACAAACAGACTTGGTAATCAAGCTTATGGACAGTGATACAGGCA 302
Db 1207 RRR 1148
QY 303 CAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGA 362
Db 1147 RRR 1088
QY 363 G 363
Db 1087 R 1087

RESULT 2
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 4.2%; Score 37.2; DB 4; Length 1141;
Best Local Similarity 8.7%; Pred. No. 0.072;
Matches 47; Conservative 235; Mismatches 259; Indels 2; Gaps 1;
QY 211 AACTACCCCTGAGTGAATGAAACTTTATCTTCACTGTGTCTGACCGGACAAACACTT 270
Db 62 ARMYKYRRYNNKSRWKGWYKKWYBCANNITSBRYHARRWKDMKTAYBMTWNKWKGT 121
QY 271 GGTAATCAAGCTTATGACAGATGATACAGCAGCAGATGACTTTGTTGGTGAAGCAAC 330
Db 122 GWRHRYWRWRMBDVTVDHHYVVTAMNNAWTTTMCMDKDDKRTWRWWKNNNATGWD DDTKY 181
QY 331 GATTTCATTGGAAGCAGTGTATGTAAGAGCACTTCACCAACACTCTATAATGTTCT 390
Db 182 HMNNNGCBTVTWVRYKTRDRBSBRMNYGMBWKNWSVDVYVWWDDMKCKVRKW 241
QY 391 GAAAGGTG--AAAAATACTGCGGGGAAATCAAAGTTGGTCTCACAATCACTCCTGAGGAT 448

Db 242 VTRGRMRNMYVAMBTAHRRYYNNGWTBAMAYRRRTWNNNNNNNAKAMCKBRAKYWGWRAB 301
QY 449 ACTCCCGCAGCGGGTCTCCAGAGACTTCGGTGTGATGGAAGCAATCATCTTAGAGCTAG 508
Db 302 VNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWKMWSAAMGVVYNNNNNNNNWYTKKAR 361
QY 509 ATGCTTTTAAGGGTGCACGAGACAGCAGCAATTCATGCGCTTGGAGCCTTCAGCCGTC 568
Db 362 HBARWDVWHSNAWKWHANAHAHYSRKKWTBYKRTWVNNNGTTWVKRWAWYWKMDMDW 421
QY 569 GAGTACTTCACTGAATCGAGAAATTCATTGCAATTTGGCTCTTTTGAATTTGTTTCAAGA 628
Db 422 BGTNNNNNGRTYTGWTKNKKOMTYKWKANNCKWRAWDHKCTCHNNTTMMKMTYWN 481
QY 629 AGTGTTATTAGTAGCTTTCAACAAAAATAGTCCATATTGCTCTATATCCCGTATTGA 688
Db 482 CYWKSMTNGKSHRBAAAVTYTWMMWRRYAHANNNNNDYMWKACTWYKYBVCSKWNYYA 541
QY 689 AATCTAAGCGCGTTTGTGATTACTGCTTACAAACAAGAGTTTGTCTTCTAGTTCCCACT 748
Db 542 AWYTKSSWNYTSRYRWKTNNSWRWSDTRSGRANNYARABHYGYKWTNRWBWSHTWB 601
QY 749 ACG 751
Db 602 HBR 604

RESULT 3
US-09-688-078-5
; Sequence 5, Application US/09688078
; Patent No. 6660483
; GENERAL INFORMATION:
; APPLICANT: Kask, Kalev
; APPLICANT: Melcher, Thorsten
; APPLICANT: Chin, Daniel J.
; TITLE OF INVENTION: DIAGNOSTIC MARKER FOR NEUROLOGICAL CONDITIONS
; FILE REFERENCE: 019488-001310US
; CURRENT APPLICATION NUMBER: US/09/688,078
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/159,622
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2958
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-688-078-5

Query Match 4.2%; Score 37.2; DB 4; Length 2958;
Best Local Similarity 50.6%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 90; Conservative 0; Indels 88; Indels 0; Gaps 0;
QY 179 GAGCAGAGAGCAGATGTTGCAACTGGAAGAAAGAACTACCCCTGAGTGAAGTGAAGT 238
Db 2105 GAACAGAGAGCGAAAACCTGTGAACAGATGGAGATGCTCTATGTTGATGAAGCTTT 2164
QY 239 ATCTTCACTGTGTCTGACCGGACAAACAGACTTGGTAAATCAAGCTTATGACAGTGA 298
Db 2165 GAAATTTCAAAATCAACCTCCCGAACTAGCCATGGTGGCGCTTTGTAGTGTGATGATG 2224
QY 299 GGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTCGGAAGCAGTGTATCTG 356
Db 2225 TACATTTGGCGATTAATTTATTGGCCAGTACAGCATTCCTTTGAATGTTTACAAACG 2282

RESULT 4
US-09-205-258-206/c
; Sequence 206, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.

US-09-799-451-554

Query Match 4.1%; Score 36; DB 4; Length 2229;
Best Local Similarity 47.7%; Pred. No. 0.29;
Matches 105; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 102 TTGGGCGGAGGCGCTCGAGAACCGGATTTACCTCTGTAAACATGATCGGTATGCAATTC 161
DB 247 TTGAAGGGAGAGACCTCAAGGCCATGGATTCACCGGGTTGAGCATCCTACGTGAGT 306
QY 162 TCAAGTGGCGGTTTACAGGAGCAGACGAGTATTCGAACTGGAAGAACTACCCCTG 221
DB 307 TCGGGCTTGGCATCAGAGTACAGCAGAGATTATGCAAAACGTTGATCTCAGT 366
QY 222 AGTGAATGAAACTTTATCTTCTCAGTGTCTGACCGGACACAGACTTGGTAATCAAGC 281
DB 367 GGAGGGAACAATTTGATTTTACCTTTATGAAGAAAGAGGAGGTGATTTGATATCAGT 426
QY 282 TTATGACAGTGTATACAGGCACAGCAGATGACTTTTCTGG 321
DB 427 CATGGGACAAAGATGCTGGGAAAGGGATGATTTCAATGG 466

RESULT 6

US-09-780-175-17
Sequence 17, Application US/09780175
Patent No. 6440738

GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier

APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION

FILE REFERENCE: RTS-0184

CURRENT APPLICATION NUMBER: US/09/780,175

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 17

LENGTH: 5917

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1634)...(1990)

NAME/KEY: CDS

LOCATION: (2876)...(2750)

NAME/KEY: CDS

LOCATION: (3344)...(3382)

NAME/KEY: CDS

LOCATION: (3969)...(3992)

NAME/KEY: CDS

LOCATION: (4185)...(4403)

NAME/KEY: CDS

LOCATION: (4670)...(4735)

US-09-780-175-17

Query Match 4.1%; Score 36; DB 4; Length 5917;
Best Local Similarity 62.0%; Pred. No. 0.57; Indels 35; Gaps 0;
Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 34 AGGGGCTTGTGAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 93
DB 3102 AGGGAGTTGGAGGGAGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3161
QY 94 GCTGCTCTGGGGCCAGGGCTCGAGAACA 125
DB 3162 TGTCTCTGTTGATGCAAGGGTCAAGAGCCCA 3193

RESULT 7

US-09-806-708B-22/c

Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:

APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)...(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FABL promoters
US-09-806-708B-22

Query Match 4.0%; Score 35.4; DB 4; Length 1141;

Best Local Similarity 8.6%; Pred. No. 0.29; Indels 0; Gaps 0;
Matches 48; Conservative 224; Mismatches 283; Indels 0; Gaps 0;

QY 70 CATGTCACGGGAGCGTCTGCTCTGCTGGGCGCAAGGCGCTCGAGAACACCGA 129
DB 681 VMRRMTNTKTRWYSTTTRHHYTGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 622
QY 130 TTACCTCTGTAACATGATCGTATGCAATTCCTCAAGTCGCGTTCACAGGACGAGAAG 189
DB 621 DGMTVRKKVKWRDITCTTYVDVWADSWWVWYANMMRCRDVYTRNNYCKSAHSVWSN 562
QY 190 CAGTATTGCACTGGAAGAACTACCCCTGAGTGAATGAAACTTTATCTTCACTGT 249
DB 561 NAMVRRYSARNSSMARWTRNNWMSBVRMRWAGTMRWNNNNNNNNNNNNNNNNNNNN 502
QY 250 GTCTGACCGGACACAGACTTGGTAATCAAGCTTATGACAGTATGACGACAGCAGCA 309
DB 501 ARBTTTVYDSCNAKSMWRGNMRAKMWAAANNNDAGAMDHWTVMGNNTMMRRAKVM 442
QY 310 TGACTTTTGTGGTGAAGCAACGATTCCTCATTGGAAGCAGTGTATATCTGAAAGGAGCATTC 369
DB 441 NMWCRRAYCCNN 382
QY 370 ACCAACACTCTATAATGTTGTGAAGGTGAAAAATACTCGCGGGAATAACAAAGTTGGTCT 429
DB 381 TNDMMWTSDBWHYTVDTMPRAWNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 322
QY 430 CACATTCCTCTGAGGATATCTCGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGA 489
DB 321 WGSAYBMAAAMSWAAGASNBVTYNWCWRTYMGKTMNTNNNNNNNNNNNNNNNNNNNN 262
QY 490 GCAATCATCTTAGAGCTAGATCTTTAAGGGTGCACGAGCAGACGACCAATTCATGG 549
DB 261 YYDTAVWTBKRNKYCYAYBYWYMGKHHWRRABHRSNNNNNNNNNNNNNNNNNNNNNN 202
QY 550 CTTGGAGCCTTCAGCGCTCGAGTACTTCATGTAATGAGAAATTCATTCGATTTGCTTC 609
DB 201 HAMRVBKWABAVGCNNNNKDRMAHHWCATNNNNNNNNNNNNNNNNNNNNNNNNNNNN 142
QY 610 TTTTCATTTGTTTCAG 624
DB 141 RDDHBARKVYWYR 127

RESULT 8

US-09-252-991A-4545

Sequence 4545, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

```
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4545
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4545

Query Match          4.0%; Score 35.2; DB 4; Length 801;
Best Local Similarity 53.7%; Pred. No. 0.27;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 56 GGACCGGAGGAGGACATGCTGCACGGACGCTGGAAGTGTGCTGGTGGGCCCAAGGCC 115
Db 109 GGGCGGAAGTGGAGATCGGTGAAGGACGGTGTGCTCGCACGTGGTGTCTCAAGGCC 168

Qy 116 CTCGAGAACACCGATTACCTCTGTAAACATGGATCCGTATGCAATTCCTCAAGTCCGTTCA 175
Db 169 CCCACGAAGATCGGACAGCAACCGCATCTACCAGTTTCCACGCTCGCGAGGATACT 228

Qy 176 CAGGAGCAGAGAGCA 191
Db 229 CCCGACCTGAATACA 244

RESULT 9
US-09-252-991A-4308/c
; Sequence 4308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4308
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4308

Query Match          4.0%; Score 35.2; DB 4; Length 969;
Best Local Similarity 53.7%; Pred. No. 0.3;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 56 GGACCGGAGGAGGACATGCTGCACGGACGCTGGAAGTGTGCTGGTGGGCCCAAGGCC 115
Db 708 GGGCGGAAGTGGAGATCGGTGAAGGACGGTGTGCTCGCACGTGGTGTCTCAAGGCC 649

Qy 116 CTCGAGAACACCGATTACCTCTGTAAACATGGATCCGTATGCAATTCCTCAAGTCCGTTCA 175
Db 648 CCCACGAAGATCGGACAGCAACCGCATCTACCAGTTTCCACGCTCGCGAGGATACT 589

Qy 176 CAGGAGCAGAGAGCA 191
Db 588 CCCGACCTGAATACA 573

RESULT 10
US-09-286-981B-24
; Sequence 24, Application US/09286981B
; Patent No. 6503511
```

```
; GENERAL INFORMATION:
; APPLICANT: Wizemann, Theresa M.
; APPLICANT: Koenig, Scott
; APPLICANT: Johnson, Leslie S
; TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines
; FILE REFERENCE: 469201-396
; CURRENT APPLICATION NUMBER: US/09/286,981B
; CURRENT FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: US 60/085,743
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA derived
; OTHER INFORMATION: from the genome of Streptococcus pneumoniae
US-09-286-981B-24

Query Match          4.0%; Score 35.2; DB 4; Length 1284;
Best Local Similarity 53.7%; Pred. No. 0.37;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 287 GACAGTGATACAGGCACAGCAGATGACTTTTGTGGTGAAGCAACGATTCATTTGGAAGCA 346
Db 733 GAAATGATCGGAAGTCTTCAGATTCTAGCGTAGGTGAAGAACTCTTCCAGGCCCATCC 792

Qy 347 GTGTATCTGAAAGGAGCATTCCACCACACTCTATATGTGTGAAAGGTGAAAAATAC 406
Db 793 CTGAACCAAGAAAAAGGTTGCAGAAGCTGAGAAGAGGTTGAAGAAGCTTAAGAAAAA 852

Qy 407 TCGCGGGGAATCAAG 422
Db 853 GCCGAGGATCAAAAAAG 868
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RESULT 11

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US-09-513-999C-10484/c
; Sequence 10484, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10484
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 36
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 266
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10484
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```
Query Match          3.9%; Score 34.2; DB 4; Length 507;
Best Local Similarity 46.9%; Pred. No. 0.42;
Matches 105; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
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QY 539 CAATTCATCGCTTGAGCCCTTCAGCCGTCGAGTACTTCATGCTAATCGAGATTCATTC 598
Db 367 CTATTGAGAAGCTGCGGGCCAGCAGCAGCCAGTACAATATGCTCGAGCATTAATTTGTCA 308
QY 599 GATTTGGCTTCTTTTGATTGTTTCAGAGAAGTGTATTAGTGAGTTTCAACAAAAATA 658
Db 307 GGCCAACTTTCACACATATTITGGCAGTTCGTGTGCATACNTGGCAGACTATCATATC 248
QY 659 GTCCATATTGCTCTATATCCCGTATTGGAATTTCTAAGCCGCTTTGTGATTAAGTCTTA 718
Db 247 CCCTCTATACGGGCATAAGCAATCTGACAAATGATATCTCTGTTGTACACGAACAT 188
QY 719 CAACAAGAGTTTGTCTTCTAGTTCACATACGCTTTTTTTGA 762
Db 187 CATCCTGTATTGGGTGTGTGTATTATTTTATCTCTGATCA 144

RESULT 12
US-09-248-796A-6167
; Sequence 6167, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6167
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6167

Query Match 3.9%; Score 34.2; DB 4; Length 1548;
Best Local Similarity 49.2%; Pred. No. 0.91;
Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 247 TGTCTCTGCGGCAACACAGACTTGGTAATCAAGCTTATGGACAGTGATACAGGCACAGC 306
Db 381 TGTCAAGATCAACCAAGACGAGAGAAATAGAGTTGCTGAACCTTAAGAACTCTCAGC 440
QY 307 AGATGACTTTGTTGGTGAAGCAACGATTCCATTGGAAAGCAGTGATATCTGAAAGGAGCAT 366
Db 441 TGCATCCGAGGTAGAAGAACAAAACTTGAAGAAAGATGCTGCTGAACAGAAATTCAGA 500
QY 367 TCCACCAACTCTATTAATGTTGAAAGGTGAATAATCTGCGGGGAATCAAGTTGG 426
Db 501 TGGAGAAGCACTCAAGGCGATGACAACTTGAAGAAACAAATCAAGAGAAACCCCAATTGA 560
QY 427 TCT 429
Db 561 ACT 563

RESULT 13
US-08-998-416-256/c
; Sequence 256, Application US/08998416
; Patent No. 6239284
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
```

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; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1225RP
; US-08-998-416-256

Query Match 3.9%; Score 33.8; DB 3; Length 710;
Best Local Similarity 49.4%; Pred. No. 0.72;
Matches 117; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 218 CTTGAGTGGAAATGAAACTTTTATCTTCACTGTGTGACCGGACAAACAGACT---TGGTA 274
Db 397 CCTGTTTGGAAACGAGACACATCCCTGCAGTTGAATAACCGGATTAACAACACTTACCTGCGC 338
QY 275 ATCAAGCTTATGGACAGTGATACAGCAGCAGATGACTTTTGGTGAAGCAACGATT 334
Db 337 ATCAAGGTCATGGATGGGATGCCGGAACAGTGACGATCTCTATTGGCACCCGACCATC 278
QY 335 CCATTGGAGCAGTGTATCTGAAAGGAGCATTCCACCAACACTCTATAATGTTGTGAAA 394
Db 277 GCTCTAGCTGAGTGGACCCACAGTGAACCCCAATGGAAGTCCAGCTAACTGGTCTCT 218
QY 395 GGTGAAAAATACTGCGGGGAAATCAAGTTGTTCTCACAATTCACCTCTGAGGATACT 451
Db 217 AACGGCGAGGACGGTGGTATTCTTACTTTGAACCTTCAAAATTTTCTCCTAGGTACACT 161

RESULT 14
US-10-204-708-86
; Sequence 86, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
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; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 86
; LENGTH: 11050
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-86

Query Match          3.9%; Score 33.8; DB 4; Length 11050;
Best Local Similarity 54.4%; Pred. No. 4.9;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 608 TCTTTTGATGTTTCAGAAGTGTATTATAGTGAGTTTCAACAAAAATAGCTCCATAT 667
Db 171 TTTTATTTATTTTGTGAAGATGTTTATAGAGAGTTGTTATATAATGAATATGTGTAT 230

Qy 668 TGCTCTATATCCCGTATTGGAATCTAAGCCGTTTGTGATTACTGCTTACACACAGAA 727
Db 231 ATATATGTAAGTGTTTAGGATAGTATTCGGTACGTAGTAAATATTCGATAAATGAGTGA 290

Qy 728 GTTTT 732
Db 291 TTTT 295

RESULT 15
US-10-027-983-11/c
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Doble
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217

; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
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; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223581)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11

Query Match          3.9%; Score 33.8; DB 4; Length 392000;
Best Local Similarity 54.4%; Pred. No. 57;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 09:17:49 ; Search time 585 Seconds
(without alignments)
8591.999 Million cell updates/sec

Title: US-09-913-569B-5

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	847.4	96.7	1129	18	US-10-425-115-144798
2	846.4	96.6	1027	16	US-10-425-114-15989
3	291.6	33.3	821	17	US-10-437-963-96494
4	267	30.5	868	18	US-10-425-115-152761
5	247.2	28.2	787	16	US-10-425-114-23609
6	228	26.0	442	16	US-10-260-238-772
7	214.6	24.5	740	17	US-10-437-963-41540
8	208.8	23.8	780	16	US-10-260-238-4944
9	199.4	22.8	804	17	US-10-767-701-11176
10	193.2	22.1	782	17	US-10-437-963-87038
11	191.8	21.9	615	9	US-09-770-149-836
12	180.2	20.6	660	18	US-10-425-115-122378

13	174.8	20.0	718	16	US-10-425-114-22597	Sequence 22597, A
14	174.8	20.0	741	16	US-10-425-114-2939	Sequence 2939, Ap
15	173.6	19.8	1294	18	US-10-425-115-106431	Sequence 106431, A
16	172	19.6	866	18	US-10-425-115-11791	Sequence 11791, A
17	171.8	19.5	856	18	US-10-425-115-11787	Sequence 11787, A
18	170.4	19.5	762	16	US-10-425-114-27551	Sequence 27551, A
19	168.2	19.2	429	16	US-10-260-238-5911	Sequence 5911, Ap
20	168	19.2	1196	18	US-10-425-115-167111	Sequence 167111, A
21	162.6	18.6	646	16	US-10-425-114-11809	Sequence 11809, A
22	108.8	12.4	441	17	US-10-437-963-33381	Sequence 33381, A
23	100.2	11.4	601	18	US-10-425-115-8248	Sequence 8248, Ap
24	77.2	8.8	523	16	US-10-424-599-110802	Sequence 110802, A
25	76.2	8.7	1617	18	US-10-425-115-165068	Sequence 165068, A
26	74.6	8.5	248	16	US-10-424-599-93308	Sequence 93308, A
27	74.2	8.5	370	11	US-09-922-293-1148	Sequence 1148, Ap
28	69.6	7.9	367	16	US-10-424-599-136395	Sequence 136395, A
29	69.6	7.9	704	17	US-10-767-701-631	Sequence 631, App
30	68.8	7.9	808	16	US-10-424-599-77758	Sequence 77758, A
31	68.4	7.8	391	11	US-09-922-293-3492	Sequence 3492, Ap
32	67.6	7.7	388	16	US-10-424-599-72831	Sequence 72831, A
33	58.8	6.7	1848	18	US-10-425-115-30879	Sequence 30879, A
34	58.2	6.6	1238	18	US-10-739-930-1595	Sequence 1595, Ap
35	57.4	6.6	840	9	US-09-938-842A-2543	Sequence 2543, Ap
36	57.4	6.6	840	11	US-09-938-842A-2543	Sequence 2543, Ap
37	55	6.3	99	9	US-09-294-093B-3721	Sequence 3721, Ap
38	49.4	5.6	159	16	US-10-424-599-53762	Sequence 53762, A
39	49.2	5.6	80	9	US-09-923-876-3209	Sequence 3209, Ap
40	49.2	5.6	80	10	US-09-923-876-3209	Sequence 3209, Ap
41	49	5.6	946	16	US-10-424-599-118274	Sequence 118274, A
42	48.8	5.6	861	17	US-10-437-963-44106	Sequence 44106, A
43	48	5.5	622	17	US-10-767-795-5525	Sequence 5525, Ap
44	47.8	5.5	385	17	US-10-767-701-11177	Sequence 11177, A
45	46.8	5.3	1515	17	US-10-437-963-50658	Sequence 50658, A

ALIGNMENTS

RESULT 1
US-10-425-115-144798
; Sequence 144798, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 144798
; LENGTH: 1129
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_63541C.1
US-10-425-115-144798

Query Match 96.7%; Score 847.4; DB 18; Length 1129;
Best Local Similarity 99.1%; Pred. No. 1.7e-253;
Matches 863; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 8 GTTCGTTACGCCACAGGCAAGGCACAGCGGCTTGTGAGGAGCGAGCGAGGAG 67
Db 221 GTTCGTTACGCCACAGGCAAGGCACAGAGGCTTGTGAGGAGCGAGCGAGGAG 280

Qy 68 GACATGGTGCACGGGACGCTGGAAGTCTCTCTGTTGGGCGCAAGGCCCTCGAGAACCC 127
Db 281 GACATGGTGCACGGGACGCTGGAGGTCTCTCTGTTGGGCGCAAGGCCCTCGAGAACCC 340

Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 96494
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94586C.1
US-10-437-963-96494

Query Match 33.3%; Score 291.6; DB 17; Length 821;
Best Local Similarity 74.9%; Pred. No. 6.6e-80;
Matches 394; Conservative 0; Mismatches 124; Indels 8; Gaps 2;

Qy 47 GGAGAGCGAGCGAGGAGGACATGGTGCACGGGACGCTGGAGTGGCTGCTGTTGGG 106
Db 66 GGGCGCGGGGAGCTGGGGAAGATGGTGAGGGGACGCTCGAGGTGCTCGTCGCGA 125

Qy 107 GCCAAGGGCTTCGAGAACACCGATTACTCTGTAAACATGGATCGGTATGCAATTTCTCAAG 166
Db 126 GCCAAGGGCTTCGAGAACACCGATTACTCTGTAAACATGGATCGGTATGCAATTTCTCAA 185

Qy 167 TGCGTTTACAGGAGCAGAGAGAGAGATTTGCAACTGCGAAAGAACTACCCCTGAGTGG 226
Db 186 TGCGCTCGCAGGAGCAG 245

Qy 227 AATGAAATTTATCTTCTACCTGTCTGACCGGACACAGACTTGGTAAATCAAGCTTATG 286
Db 246 AACGAAACCTTTATGTCAGGCTCACTCAACAGCTACAGAGCTCATCATCAAGTTGATG 305

Qy 287 GACAGTGATACAGCAGCAGAGATGACTTTTGGTGAAGCAACAGTTCCATTGGAAGCA 346
Db 306 GACAGTGATGACAGCAGGATGATTTTGGTGAAGCAACAGTTTCTTTGGAAGCA 365

Qy 347 GTGTATTAAGAGGAGATTCACCAACACTCTATATGTTGTAAGGTGAAATAAC 406
Db 366 ATCTATACAGAGGAGCATACCCCAACTGTTTATATGTTGTAAGGAGAGAGATAC 425

Qy 407 TGCGGGAAATCAAGTTGTTCTACATTTACTCTGAGGATCTCCAGCGGGGTCTC 466
Db 426 CGTGGAATAATCAAAGTGGGCTGACGTTCACTCAGAGGATGATCGCGTGGGTTTA 485

Qy 467 CCAGG---GACTTCGGTGGATGAAGCAATCATCTT-----AGAGCTAGATGCTTTAAG 518
Db 486 TCTGAGGAAGCATTTGTTGATGAGAGCATCTCTTGGAGAGAGAGAGATCTTTGAT 545

Qy 519 GGTGCACAGCAGCAGCAGCAATTCATTCGCTTGGAGCTTCAGC 564
Db 546 GTGCACTGCATCGTATGTTAGTCTGTTGCTGTAAGCTTGAAC 591

RESULT 4

US-10-425-115-152761
; Sequence 152761, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

RESULT 5
US-10-425-114-23609
; Sequence 23609, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 152761
; LENGTH: 868
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70901C.1
US-10-425-115-152761

Query Match 30.5%; Score 267; DB 18; Length 868;
Best Local Similarity 72.3%; Pred. No. 3.3e-72;
Matches 361; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

Qy 60 CGGAGGAGGACATGGTGCACGGGACGCTGGAAGTGTCTGCTGGGGCCCAAGGGCTCG 119
Db 234 CCGAGAGAGATGGCGCAGGGGACGCTGGAGGTGCTGCTCGGAGCCCAAGGGACTCG 293

Qy 120 AGAACACCGATTACTCTGTAAACATGGATCGGTATGCAATTTCTCAAGTCCGTTACAGG 179
Db 294 AGAACACCGACTACTCTGTCAACATGGACCCGTACGCGGTTCTAAAAATGCACATCGCAGG 353

Qy 180 AGCAGAGAGCAGTATTGCAACTGGAAGAGAACTACCCCTGAGTGGAAATGAAAACCTTTA 239
Db 354 AGCAGAGAGCAGCGCTGCGCTCAGGAAGGAAGTATCTCTGAATGGAACGAAACCTTTG 413

Qy 240 TCTTCACTGTGTCTGACCGGACCAACAGACTTGGTAAATCAAGCTTATGGACAGTGATACAG 299
Db 414 TGTTCACGCTCTCTGAGAATGCAACCGAGCTGCTCATCAAGCTCTCGACAGTGTGGTG 473

Qy 300 GCACAGCAGATGATTTGTTGGTGAAGCAACGATTCATTGGAAGCAGTGTATCTGAAA 359
Db 474 GCACGAGCAGCAGCAGCGTTGGTGAAGCAACGATCCCATTTGGATGGAGTGTACACTGAAG 533

Qy 360 GGAGCATTCACCAACACTCTATANTGTTGTAAGGTGAAAATTAATCTCGGGGAATCA 419
Db 534 GAAGCATCCCAACACTGTTTACAATGTTGTAAGAGCAAGAGATACCGTGGGAGAAATCA 593

Qy 420 AAGTGTGTCTCACTTCACTCTGAGGATCTCGCAGCGGGGTCTCCAGAGG---ACT 476
Db 594 AATTCGTCTGACGTTCACTCCGAGGAGGCTGCTGATGAGGATCAACCGAGGAAACT 653

Qy 477 TCGGTGGATGGAAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCCACAGACAGC 536
Db 654 ACGGTGGTGGAAACCAATCATCTTGAGAAGAGTAGGTGCTTTGCTGAACACTGTGGTGGT 713

Qy 537 GACAATTCATGCGCTTGA 555
Db 714 GACAAGTCGTGCTAGAA 732

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; SEQ ID NO 23609
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB597-068-A11_FLI
US-10-425-114-23609

Query Match      28.2%; Score 247.2; DB 16; Length 787;
Best Local Similarity 76.5%; Pred. No. 4.8e-66;
Matches 303; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 52 GCAGAGAGCGGAGGAGACATGTGACGGGAGCGCTGGAGTCTGCTCGTTGGGCGCAA 111
DB 60 GCTAACCGCGGAGGAGAGATGGCGAGGGGAGCGCTGGAGGTCTTCTCGTGGGAGCCAG 119

QY 112 GGCCTCTCGAAGAACACCGATTACCTCTGTAACTGGATCCGTATGCAATTTCTCAAGTCCG 171
DB 120 GGGCTCTCGAAGAACACCGATTACCTGTAGCAACATGGACCCCTACGCGCTTCTGCAATGTG 179

QY 172 TTCACAGGAGCAGAGAGAGATTTGCAACTGCGAAAGAACTACCCCTGAGTGGAAATGA 231
DB 180 CTCCACGAGCAGAGAGAGAGCGTGCATCTGGCAAAAGGCTGTGAACCTGAGTGGAAACGA 239

QY 232 AACTTTATCTTCACTGTCTGACCGGCAACAGACTTGGTAATCAAGCTTATGGACAG 291
DB 240 GACCTTCTGTGTTTACCGTCTCCGATGGCGCAGCAGAGCTGTTTCAATCAAGCTTCTGGACAG 299

QY 292 TGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTCCATTTGGAAGCAGTGTA 351
DB 300 TGACGCTGGCAGTGTGACGATTTGTTGGTGAAGCAACGATTCTCTGGAAGCAGTTTA 359

QY 352 TACTGAAGAGGAGCATTCACCAACACTCTATATATTTGTGAAGGTGAAATATCTGCCG 411
DB 360 CACGGAAGGAACATCCCTCCGACTGTTTACAATGTTGTGAAGAGCAAGAAATACCGCGG 419

QY 412 GGAATCAAAAGTTGCTCTACATTTCACTCTCGTAGGA 447
DB 420 AGAATCAAAAGTTGGCTCCGCTCAGTTTCACTCCAGAGGA 455
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RESULT 6
US-10-260-238-772
; Sequence 772, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 772
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-772
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Query Match      26.0%; Score 228; DB 16; Length 442;
Best Local Similarity 78.6%; Pred. No. 3.4e-60;
Matches 330; Conservative 0; Mismatches 45; Indels 45; Gaps 3;

QY 71 ATGGTGACACGGGACGCTGGAAAGTCTGCTGTTGGGGCCCAAGGCGCTTCGAGAACACCGAT 130
DB 1 ATGGTGACACGGGACGCTGGAGGTGCTGCTCGTGGGGCCCAAGGCGCTTCGAGAACACCGAT 60

QY 131 TACCTCTGT-----ACATGGA 147
DB 61 TACCTGTGTACGCATCAGCTTATAATTCCTAATCCTTTAAAGCGCATTTGCTTTGAACATGGA 120

QY 148 TCCGTATGCATTTCTCAAGTGCCTTTCACAGGACAGAGAGAGTATTGCAAC-TGGAA 206
DB 121 TCCATATGCATTTCTCAAGTGCCTTTCACAGGACAGAGAGAGCATAGCATCAGGGCA 180

QY 207 AAGGAATACCCCTGAGTGGAAATGAAACTTTATCTTCTGCTGTGTCGACCGGCAACAG 266
DB 181 AAGGAAGTAACCCCTGAATGGAAACGAAACTTTTGTCTTCCCGTGTCTGACAAAGCTACAG 240

QY 267 ACTTGGTAAATCAAGCTTATGGACAGTATACAGGACAGCAGATGACTTTCTGTTGGTGAAG 326
DB 241 AGCTGTTGATCAAGCTCTTGGACAGTATGCTGCTCAGCCGAGCACTTTGTTGGTGAAG 300

QY 327 CAACGATTCCCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCAACACTCTATATATG 386
DB 301 CAAC-ATTCTTTTGAAGCAGTGTATCTGAAAGGAGTATTCCACCAACTCTGTATATATG 359

QY 387 TTGTGAAAGGTGAAAAATACCTGCGGGGAAATCAAAAGTTGGTCTCACATTCCTCTGAGG 446
DB 360 TTGTGAAGGATGAACATTACTGTGGAGAAATCAAAAGTCGGCTCACATTCCTCTGAGG 419
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RESULT 7
US-10-437-963-41540/c
; Sequence 41540, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41540
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44875C.1
US-10-437-963-41540
```

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Query Match      24.5%; Score 214.6; DB 17; Length 740;
Best Local Similarity 78.8%; Pred. No. 7.1e-56;
Matches 256; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 189 GCAGTATTCGAACCTGGAAGGAAGTACCCCTGAGTGGAAATGAAATTTATCTTCTCAGCTG 248
DB 598 GCTATGTGATTGTGGCAAAAGGAAGTAACCTGATGGAAACGAAACTTTGTTCTTCCCG 539

QY 249 TGTCTGACCGGACACAGACTTTGGTAATCAAGCTTATGGACAGTGTATGACAGGACAGCAG 308
DB 538 TGTCTGACAAAGCTACAGAGCTTTGATCAAGCTCTTGGCCAGTGTACTGCTCACCAG 479
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Qy	309	ATGACTTTTGGTGAAGCAACGATTCATTGGGAAGCAGTGTATATCTGAAAGGAGGATTC	368
Db	478	ACGACTTTTGGTGAAGCAACGATTCCTTTTGGAAACCAAGTGTATATCTGAAGGGAGTATTC	419
Qy	369	CACCAACACTCTATAACTGTTGGAAGGTGAAAATACTCGCGGGAAATCAAAGTTGGTC	428
Db	418	CCCACTCTGTATATGTTGTGAAGATGACCATTCCTGTGGAGAAATCAAAGTCGGGCC	359
Qy	429	TCACATTCACCTCTGAGGATACTCGCCACGCGGGTCTCCACAGGACTTCGGTGGATGA	488
Db	358	TCCCATTCCTCTGAGGATGTTCCGACGCGTGGTCTTCTCTGAGGACTTTGGTGGATGA	299
Qy	489	AGCAATCATCTTAGAGCTAGATGCT	513
Db	298	AGCAATCTCGTTAAAAAAGCAGAT	274

```

RESULT 8
US-10-260-238-4944/c
; Sequence 4944, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, FumiYaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260.238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 4944
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Musa acuminata
US-10-260-238-4944

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Query Match	23.8%;	Score 208.8;	DB 16;	Length 780;
Best Local Similarity	68.5%;	Pred. No. 4.8e-54;		
Matches 304;	Conservative 0;	Mismatches 137;	Indels 3;	Gaps 1;
Qy	71	ATG	TG	CACGGGACGCTGGAAAGTCCTGCTCTGTTGGGGCCAAAGGCGCTCGAGAACACCGAT 130.
Db	757	ATG	TTCTCGGAACGCTGGAGGTCTGCTCTGAGCGCCAAAGGCGCTCGAGGACGTCGAT 698	
Qy	131	TAC	CTCTGTACATGGATCCGTATGCAATCTCTCAAGTCCCGTTTACAGGAGCAGAAAGC 190	
Db	697	TTCTTCGGCAAAATGGATCTCTTATGCGGCTCTTACGTACCGCAGTCAGGAACAGAAAAGC 638		
Qy	191	AGT	ATTTCGAATCGAAAAAGGAACCTACCCCTCAGTGGAAATGAAAACCTTTATCTTCACGTGTG 250	
Db	637	AGT	ACTGCATCAGTGCAGGTAGTAAATCTCTGAATGGAAATGAGACCTTTGCTTTTAATGTG 578	
Qy	251	TCT	GACCGGACAAACAGACTTGGTAAATCAAGCTTATGGACAGTGTATGAGGCACACGAGAT 310	
Db	577	TCT	GACAAATGCTCGGAGCTCATTTGTTAAATCATGACACAGTGATACTTTTTCAAAAGAT 518	
Qy	311	GAC	TTTGTGGTGAAGCAACGATTTCCATTTGGAACAGTGTATATCTGAAAGGAGCATTTCCA 370	
Db	517	GAT	TTCTGTAGAGAAAGCAAAAATCCCATTTGGAACAGTGTTCGTGGAAAGGAAGCCTCAGC 458	

[illegible]

```

RESULT 9
US-10-767-701-11176
; Sequence 11176, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhao, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Mo
; TITLE OF INVENTION: Plants and Uses Thereof For Plant
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 11176
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS15003_1
US-10-767-701-11176

```

Query Match	22.8%	Score 199.4	DB 17	Length 804
Best Local Similarity	70.3%	Pred. No. 4.2e-51		
Matches 282	Conservative 0	Mismatches 116	Indels 3	Gaps 1
Qy	47	GGAGAGCGAGGAGCGGAGGAGGACATGCTGCACGGGACGCTGGGAAGTGCCTCTCGTGGG	106	
Db	142	GGAACACAGCACCGGGGCGCAACATGGTTACAGGGGAAGCTTGAGGTCCTCTCTGCTCC	201	
Qy	107	GCCAAGGGCCTCGAGAACACCGATTAACCTCTGTAAACATGGATTCGGATTCGAATTCCTCAAG	166	
Db	202	GCCAAGGGCCTCGAGGACACCGATTTCTCTCAATAACATGGACCCCTTCCTGTATCCTTACA	261	
Qy	167	TGCGGTTCAGGAGCAGAGGACGATATGCCAACTCGMAAAGGAACTACCCCTCAGTGG	226	
Db	262	TGCCGCACACAGGAGCAAGAAAGCAGCGTTCGAAATGGAGCAGGAATGAGCGCTGAAATGG	321	
Qy	227	AATGMAAACTTTATCTTCACCTGTCTGCACGGCAACACAGACTTGGTAAATCAAGCTTATG	286	
Db	322	AACGAGACCTTCATCTTCACCGTCTCTGATGAACCCCGCAGCTCCATCTCAAGATCATG	381	
Qy	287	GACAGTGATACAGGCACAGCAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCA	346	
Db	382	GACAGCGAT---GTCACTAACGATGATTTTGTGGTGAAGCAACCATCCCTCTGGAGGTT	438	
Qy	347	GTGTATACTGAAAGGAGCATTCCACCAACACTCTATAATGTGTGMAAGGTTGMAAAATAC	406	
Db	439	GTGTTTCAGGAGGACAGCCCTCTCCGGCAGTTGTCATCCGTCGTCNAGGAGGAGGAATAC	498	
Qy	407	TGCGGGGAAATCAAAGTTGGTCTCACATTCACCTCCTGAGGA	447	
Db	499	TGCGGAGAGATCAAGCTTTGCACTCACCTTCACTCCAGCAGA	539	

RESULT 10
US-10-437-963-87038
; Sequence 87038, Application US/10437963
; Publication No. US20040123343A1


```
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 122378
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_43093C.1
US-10-425-115-122378

Query Match
Best Local Similarity 20.6%; Score 180.2; DB 18; Length 660;
Matches 263; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy 47 GGAGAGCGAGGCGGAGGAGACATGCTGACCGGACGCTGGAAGTCTGCTGTTGGG 106
Db 39 GGAGATCGAAGAGGAGGAGAGACATGCTGCGCGGAGAGCTGGAGTCTGCTCTCC 98

Qy 107 GCCAAGGCGCTCGAAGACACCGATTACTCTGTAACTGATCGTATGCAATTCCTAG 166
Db 99 GCCAAGGCGCTCGAAGACACCGATTACTCTGTAACTGATCGTATGCAATTCCTAG 158

Qy 167 TGCCGTTTACAGAGGAGGAGAGAGATTCGAACTGAAAGAACTACCCCTGAGTGG 226
Db 159 TGCCGAGCCACAGAGGAGAGAGAGAGATTCGAACTGAAAGAACTACCCCTGAGTGG 218

Qy 227 AATGAAATCTTATCTTCTACCTGTCTGACCGGACAAACAGACTTGGTAATCAAGCTTATG 286
Db 219 AATGAGACCTTCTTCTTCCGCACTCTCCGCGACGCTCCGGAGCTCAGGTCAGATCATG 278

Qy 287 GACAGTATACAGGACAGCAGATGACTTTTGGTGAAGCAACAGATTCATTTGGAAGCA 346
Db 279 GACAGCAGCGCTCTCGGCGAGAGAGCTCTGTCGGAAGAGATGCATCCCGCTGGAGCG 338

Qy 347 GTGTATCTGAAAGAGAGATTCACCAACACTCTATATGTTGTAAGGTGAAATAC 406
Db 339 GTGCTTCAGGAGGAGAGAGCTCCCGCGGCGCTGACCGGCTGTCAGAGGAGGAGTAC 398

Qy 407 TGCGGGAATCAAAGTTGGTCTCACAATTCACCTCTCTGAGGA 447
Db 399 CGCGAGAGATCAAGATCGGCTCACCTTCAACCCCGGAGCA 439

RESULT 13
US-10-425-114-22597
; Sequence 22597, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22597
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-005-D8_FLI
US-10-425-114-22597

Query Match
Best Local Similarity 20.0%; Score 174.8; DB 16; Length 718;
Matches 264; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 50 GAGCGAGGCGGAGGAGGAGATGCTGACCGGACGCTGGAAGTCTGCTGTTGGGGCC 109
Db 111 GATCGGGGCAAGGAGATAAACATGTCACGGGAAGCTGGAGGTCTCTCTCTCGCC 170

Qy 110 AAGGGCTTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTTCTCAAGTGC 169
Db 171 AAGGACTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCTTACCTGC 230

Qy 170 CGTTTCAGGAGCAGAGAGCAGTATTTGCAACTGGAAAGAACTACCCCTGAGTGAAT 229
Db 231 CGCACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290

Qy 230 GAAATCTTATCTTCTACTGCTGTCGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
Db 291 GAGACCTTCTGCTTTCACCGCTCCGACGACACCCCGCAGCTTCCACCTTCAAGATCATGAC 350

Qy 290 AGTGATACAGGACAGCAGATGACTTTGTTGGTGAAGCAACGATTTCCATTTGGAAGCAGTG 349
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Db 81 GATCGGGCAAGGAGATATAACATGTCACCGGAAGTGGAGGTCTCTCTCTCTCGCC 140
Qy 110 AAGGGCTTCGAGAACACCGATTACCTCTGTAAACATGATCGTATGCAATTTCTCAAGTGC 169
Db 141 AAGGACTCGAGGACACCGATTTCCTCAATAACATGACCCCTTCGTGATCTTACCTGC 200
Qy 170 CGTTTCAGGAGCAGAGAGCAGTATTTGCAACTGGAAGAACTACCCCTGAGTGAAT 229
Db 201 CGCACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 260
Qy 230 GAAATCTTATCTTCTACTGCTGTCGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
Db 261 GAGACCTTCTGCTTTCACCGCTCCGACGACACCCCGCAGCTTCCACCTCAAGATCATGAC 320
Qy 290 AGTGATACAGGACAGCAGATGACTTTGTTGGTGAAGCAACAGATTTCCATTTGGAAGCAGTG 349
Db 321 AGCA---CCTCAACAGCAGATTTCTGTCGGGAGCAACCATCCCTTGGAGCGCGTG 377
Qy 350 TATACTGAAAGGAGCATTCCACCAACTCTATATGTTGTGAAGGTGAAAAATATCTGC 409
Db 378 TTTCAGGAAGGAGCGCTTCCCGCGGTTTCAACCGGTCGTCAGGAGGAGAGTACTGTC 437
Qy 410 GGGGAATCAAAGTTGCTCTCACATTCACCTCTG 443
Db 438 GGAGAGTCAAGCTCGCGCTCACCTTCACTCCAG 471

RESULT 14
US-10-425-114-2939
; Sequence 2939, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2939
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237789_FLI
US-10-425-114-2939

Query Match
Best Local Similarity 20.0%; Score 174.8; DB 16; Length 741;
Matches 264; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

Qy 50 GAGCGAGGCGGAGGAGGAGATGCTGACCGGACGCTGGAAGTCTGCTGTTGGGGCC 109
Db 111 GATCGGGGCAAGGAGATAAACATGTCACGGGAAGCTGGAGGTCTCTCTCTCGCC 170

Qy 110 AAGGGCTTCGAGAACACCGATTACCTCTGTAACATGGATCCGTATGCAATTTCTCAAGTGC 169
Db 171 AAGGACTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCTTACCTGC 230

Qy 170 CGTTTCAGGAGCAGAGAGCAGTATTTGCAACTGGAAAGAACTACCCCTGAGTGAAT 229
Db 231 CGCACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 290

Qy 230 GAAATCTTATCTTCTACTGCTGTCGACCGGACCAACAGACTTGGTAATCAAGCTTATGAC 289
Db 291 GAGACCTTCTGCTTTCACCGCTCCGACGACACCCCGCAGCTTCCACCTTCAAGATCATGAC 350

Qy 290 AGTGATACAGGACAGCAGATGACTTTGTTGGTGAAGCAACGATTTCCATTTGGAAGCAGTG 349
```

Db 351 AGCGA---CCTCACCACGACGATTTCGTGCGCGAAGCAACCATCCCTCTGGAGGCCGTG 407
QY 350 TATACTGAAGAGGAGATTCCACCAACTCTATATGTGTGAAAGGTGAAAAATACTGC 409
Db 408 TTTCAGGAAGGACGCGCTTCCCGCGCGGTTTCCCGGTTCGTCAAGGAGGAGAGTACTGC 467
QY 410 GGGGAAATCAAAGTTGGTCTCACATTCACTCCTG 443
Db 468 GGAGAGGTCAAGCTCGCGCTCACCTTCACTCCAG 501

RESULT 15

US-10-425-115-106431
; Sequence 106431, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 106431
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_28567C.1
US-10-425-115-106431

Query Match 19.8%; Score 173.6; DB 18; Length 1294;
Best Local Similarity 67.3%; Pred. No. 6.5e-43;
Matches 261; Conservative 0; Mismatches 124; Indels 3; Gaps 1;
QY 56 GGAGCGGAGGAGGACATGGTGACGGGACGCTGGAGTGTCTGCTGGGGCCCAAGGGC 115
Db 665 GGGAGGAGATAAATGGTGACGGGAGCTGGAGGTCTCTCTCCGCCAAGGGA 724
QY 116 CTCGAGAACACCGATTACCTCTGTAAATGGATCCCGTATGCAATTCCTCAAGTGCCCGTTCA 175
Db 725 CTCGAGGACACCGATTTCCTCAATAACATGGACCCCTTCGTGATCCTTACCTGCCGCACC 784
QY 176 CAGGAGCAGAGAGCAGTATTGCAACTGGAAGGAACTACCCCTGAGTGGAAATGAAAC 235
Db 785 CAAGAGCAGAAAGCAGCGTCGCAATGGAGCAGGAAGCGAGCCCGAGTGAACGAGACC 844
QY 236 TTTATCTTCACTGTGTGACCGGACACAGACTTCGTAATCAAGCTTATGGACAGTGAT 295
Db 845 TTGCTCTTCACTGTCTCCGAGCAGACCCCGAGCTCCACCTCAAGATCATGGACAGCGAT 904
QY 296 ACAGGCACAGCAGATGACTTTGTGTGTAAGCAACGATTCCATTGGAGCAGTGTATACT 355
Db 905 ---CTCACCACACGACGATTTCGTGCGGCGAAGCAACCATCCCTGGAGGCCGTGTTTCA 961
QY 356 GAAAGGAGCATTCACCAACACTCTATATGTGTGAAAGGTGAAAAATACTGCGGGGAA 415
Db 962 GAAGGAGCGCTTCCCGCGCGGTTCACCGCGGTTCAGGAGGAGGAAGTACTGCGGAGAG 1021
QY 416 ATCAAAGTTGGTCTCACATTCACTCCTG 443
Db 1022 GTCAAGCTCGCGCTCACCTTCACTCCAG 1049

Search completed: January 8, 2005, 11:49:11
Job time : 588 secs

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Qy 373 AACACTCTATATGTTGTGAAGGTGAAATAATCTCGGGGAAATCAAAGTTGGTCTCAC 432
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 301 AACTGTTTATATGTTGTGAAGAGAGATACCGTGGAGAAATCAAAGTGGCCCTGAC 360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 433 ATTCACCTCCTGAGGATCTCGCCAGCGGGGTCTCCAGAG---GACTTCGGTGGATGGAA 489
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 361 GTTCACTCCAGAGGATGATCGCGATCGGGGTTTATCTGAGGAAGACATTGGTGGATGGAA 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 490 GCAATCATCTT-----AGAGCTAGATGCTTTAAGGGTGCACCAGAGCAGCGACAATTC 544
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 421 GCAGTCATCTTGAGGAAGAGCAGATACTTTGATGTGCGCACTGCATCGCTATGGTAAGTC 480
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 545 ATGCGCTTGGAGC 557
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 481 GTGTGCTGGAACC 493
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: January 8, 2005, 09:17:44
Job time : 3413 secs

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Qy 481 TGGATGGAAGCAATCATCTTA 501
Db 345 TGGATGGAAGCAATCTCGTTA 325

RESULT 14
CF335095 540 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--04-K06.bi AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-K06, mRNA sequence.
CF335095
CF335095.1 GI:33818529
EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 540)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..540
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-K06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN
Query Match 32.4%; Score 284.2; DB 6; Length 540;
Best Local Similarity 77.9%; Pred. No. 4.8e-73;
Matches 356; Conservative 0; Mismatches 98; Indels 3; Gaps 1;

Qy 47 GGAGCGAGGAGCGGAGGAGACATGGTGCACGGGACGCTGGAGAGTGTCTGTTGGG 106
Db 3 GGGCGCGGGGAGCTGGGGAAGATGGTGCAGGGACGCTCGAGGTGTCTGTCGGA 62

Qy 107 GCCAAGGGCTCGAGACACCGATTACTCTGTAAACATGGATCGGTATGCAATTTCTCAAG 166
Db 63 GCCAAGGGCTCGAGACACCGATTACTCTGTAAACATGGATCGGTATGCAATTTCTCAAA 122

Qy 167 TCCCGTTACAGGAGCAGACGAGTATTGCAACTGGAAAGAACTACCCCTGAGTGG 226
Db 123 TCCCGTTCCGAGAGCAGAGCAGCGTTCGTCAGTAAAGATCTGACCTGGAATGG 182

Qy 227 AATGAAACCTTATCTTCTCAGTGTCTGACCGGACACAGACTTTGGTAAATCAAGCTTATG 286
Db 183 AACGAAACCTTATGTTTCAGCGTCACTACACACGCTACAGAGCTCATCATCAAGTTGATG 242

Qy 287 GACAGTATACGACGACGAGATGACTTTGTTGGTGAAGCAACGATTCATTGGAAGCA 346
Db 243 GACAGTGAAGTGGCAGCGGATGATGATTTGTTGGAGAAACACGATTTCTTTGGAAGCA 302

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Qy 347 GTGTATACTGAAGGAGCATTCACCAACACTCTATATGTTGTGAAGGTGAAAAATAC 406
Db 303 ATCTATACAGAGGAAGCATACCCCAACTGTTTATATGTTGTGAAGGAAGAAATAC 362

Qy 407 TCGGGGAAATCAAAGTTGTTCTACATTCACTCTCAGGATACCTCCACGCGGGTCTC 466
Db 363 CGTGGAAATCAAAGTGGCGCTGACGTTCACTCCAGAGGATGATCGGATCGGGTTTA 422

Qy 467 CCAGAG---CAGTTCGGTGGATGGAACCAATCATCTT 500
Db 423 TCTGAGGAAGACATTTGGTGGATGGAAGCAGTCATCTT 459

RESULT 15
D23846 676 bp mRNA linear EST 03-APR-2002
LOCUS RICR0374A Rice root Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone R0374, mRNA sequence.
D23846 AU031663
D23846.2 GI:15072279
EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 676)
AUTHORS Minobe, Y. and Sasaki, T.
TITLE Rice cDNA from root
JOURNAL Unpublished (1995)
COMMENT On Dec 2, 1993 this sequence version replaced gi:427711 gi:3767636.
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
FEATURES
source
1..676
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="R0374"
/clone_lib="Rice root"
/notes="Prepared from seedling root."

ORIGIN
Query Match 31.9%; Score 279.4; DB 7; Length 676;
Best Local Similarity 75.9%; Pred. No. 1.4e-71;
Matches 374; Conservative 0; Mismatches 111; Indels 8; Gaps 2;

Qy 73 GGTGACGGGACCGCTGGAAGTGTCTGCTGGGGCCAGGGCTCGAGAACCCGATTA 132
Db 1 GGTGACGGGACCGCTCGAGTGTCTGCTCGGAGCAAGGGCTCGAGAACCCGACTA 60

Qy 133 CCTCTGTAACATGGATCCGTTATGCAATTTCTCAAAGTCCGTTTCAAGAGCAGAGAGCAG 192
Db 61 CCTGTGCAACATGGACCCGTTACGCGGTTCTCAATGCCGCTCGCAGAGCAGAGAGCAG 120

Qy 193 TATTGCAACTGGAAGGAACCTACCCCTGAGTGGAAATGAAAATTTTATCTTCTGTC 252
Db 121 CGTTGCGTCAGGTAAAGGATCTGACCTGAAATGGAACGAAACCTTTTATGTTTCAGCGTCAC 180

Qy 253 TGACCGGACAAACAGACTTGGTATCAAGCTTATGGACAGTGATACAGGCACACAGATGA 312
Db 181 TCACAAAGCTACAGAGCTCATCATCAAGTTGATGGACAGTGACAGTGGCAGCGATGATGA 240

Qy 313 CTTTGTGTTGAAGCAACGATTCATTTGGAAGCAGTGTATCTACTGTAAGAGGAGCATTCACCC 372
Db 241 TTTTGTGGAAGCAACGATTTCTTTGGAAGCAATCTATACAGAGGAGCATACCCCC 300

```


(japonica cultivar-group)], mRNA sequence.

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ACCESSION   CA755886
VERSION     CA755886.1  GI:25799925
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 622)
AUTHORS    Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
            Ferreira,H., Kawasaki,S., McColough,A., Michalowski,C.B.,
            Palacio,C., Scara,G., Wheeler,M. and Zepeda,G.R.
            Functional Genomics of Plant Stress Tolerance
            Unpublished (2000)
            Contact: Mark Fredrickson
            Department of Plant Biology
            University of Illinois
            1201 W. Gregory Dr., Urbana, IL 61801, USA
            Tel: 2172655473
            Email: bohnertlab@life.uiuc.edu.
FEATURES             Location/Qualifiers
     source          1..622
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="BR030030000.PLATE_E11_85_086.ab1"
                     /tissue_type="roots"
                     /dev_stage="3-4 weeks"
                     /clone_lib="OA"
                     /notes="19 h 200mM NaCl"

ORIGIN
Query Match      33.0%; Score 289.4; DB 6; Length 622;
Best Local Similarity 74.9%; Pred. No. 1.4e-74;
Matches 390; Conservative 0; Mismatches 123; Indels 8; Gaps 2;

QY  47  GGAGACGAGGAGCGGAGGAGGAGGATGGTCACGGGACGCTGGAAGTGTGCTGCTGGG 106
DB  51  GGGGCGCGGGGAGCTGGGAAGATGGTGCGAGGAGCGCTCGAGTGTGCTGCTGGGA 110
QY  107  GCCAAGGGCTCGAGAACCCGATTACCTCTGTGAACATGGATCCGATGCAATTTCTCAAG 166
DB  111  GCCAAGGGCTCGAGAACCCGACTACCTGTGCAACATGGACCGTACGGGTTCTCAA 170
QY  167  TGGCGTTTCAGAGAGAGAGACGATTTGCACTGGAAAGGAACCTACCCCTGAGTGG 226
DB  171  TGGCGCTCGCAGGAGCAGAGCAGCGTTGGCTCAGGTAAAGGATCTGACCCCTGAATGG 230
QY  227  AATGAAACCTTTATCTTCACTGTCTGACCGGACACAGACTTGGTATATCAAGCTTATG 286
DB  231  AACGAAACCTTTATGTTACGCTCACTCAACGCTACAGAGCTCATCATCAAGTTGATG 290
QY  287  GACAGTGATACAGGCACAGCAGATGATTTGTTGGTGAAGCAACGATTCATTTGGAAGCA 346
DB  291  GACAGTGATACAGGCACAGCAGATGATTTGTTGGAGAGCAACGATTTCTTTGGAAGCA 350
QY  347  GTGTATCTAGAAAGGAGCATTCCACCAACACTCTATAATGTTGTGAAGGTGAATAATAC 406
DB  351  ATCTATACAGAGGAAGCATACCCCNACTGTTTATTAATGTTGTGAAGGAAGAATATAC 410
QY  407  TGGGGGAATCAAGTGTGCTCACTTCATCTCCTGAGGATATCGCCAGCGGGGTCTC 466
DB  411  CGTGAGGAATCANAGTGGCCCTGAGCTTCACCTCCAGAGGATGATCCGATCGGGGTTTA 470
QY  467  CCAGAG- -GACTTCGGTGGATGGAAGCAATCATCTT- -AGAGCTAGATGCTTTAAG 518
DB  471  TCTGAGGAAGACATTCGTTGGATGGAAGCAGTCACTTTGAGGAAGAGCAGATCTTTGAT 530
QY  519  GGTGCAACGAGCAGACGACAAATTCATGCGGTTGGAGCCT 559
DB  531  GTGCACTGCATCGCTATGTTAGTGTGTTGCTGTTGGAAGCCT 571
```

RESULT 13
CA759891/c

LOCUS
DEFINITION

CA759891.1 705 bp mRNA linear EST 27-NOV-2002
BR060013A20H04.ab1 clones Oryza sativa (indica cultivar-group)
CDNA clone BR060013A20H04.ab1 similar to elicitor-responsive gene 3
[imported] - rice, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

CA759891.1 GI:25803930
EST.
Oryza sativa (indica cultivar-group)

SOURCE
ORGANISM

Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS

Bennett,J., Arumugam,K., Lafitte,R., Wen,J. and Bruskiewich,R.
Rice Microarray
Unpublished (2002)

TITLE
JOURNAL

Contact: Mark Fredrickson
Department of Plant Biology
University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473

Email: bohnertlab@life.uiuc.edu
http://www.iris.irri.org).

COMMENT

International Rice Information System (IRIS);
http://www.iris.irri.org).

FEATURES
source

1..705
/organism="Oryza sativa (indica cultivar-group)"

/mol_type="mRNA"

/cultivar="IR64"

/db_xref="taxon:39946"

/clone="BR060013A20H04.ab1"

/tissue_type="Panicles"

/dev_stage="Flowering"

/clone_lib="IRRI clones"

/note="Vector: pBluescript II SK+; Water stress was
applied by not watering for 4 consecutive days. Panicles
were collected from control (well watered) and stressed
plants at 2 days before heading, heading, 50% flowering
and 4 days after 50% flowering."

ORIGIN

Query Match 32.5%; Score 285; DB 6; Length 705;
Best Local Similarity 84.3%; Pred. No. 3e-73;

Matches 321; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 121 GAACACCGATTACCTCTGTAAACATGGATCCGATGCAATTTCTCAAGTGCCTTACAGGA 180

DB 705 GAACACCGATTACCTCTGTAAACATGGATCCGATGCAATTTCTCAAGTGCCTTACAGGA 646

QY 181 GCAGAGAGCAGTATTGCAACTGGAAAGAACTACCCCTGAGTGGAAATGAAAACTTTAT 240

DB 645 GCAGAGAGCAGCAGTATTGCAACTGGAAAGAACTACCCCTGAGTGGAAATGAAAACTTTGT 586

QY 241 CTTCACTGTCTGACCGGACCAACAGACTTGTATCAAGCTTATGGACAGTATACAGG 300

DB 585 CTTCCCGGTCTGACAAAGCTTACAGAGCTGTGTATCAAGCTTCTGGACAGTATACAGG 526

QY 301 CACACAGATGACTTTGTTGGTGAAGCAACGATTCATTTGGAAGCAGTGTATATCTGAAAG 360

DB 525 CTCACGCCAGCATTTGTTGGTGAAGCAACGATTCCTTTGGGAAGCAGTGTATATCTGAAAG 466

QY 361 GAGCATTTCCACCAACACTCTATAATGTTGTGAAGGTGAAATAATCTCGCGGAAATCAA 420

DB 465 GAGTATTTCCCCCAACTCTGTATAATGTTGTGAAGGATGAACATTTCTGTGGAGAAATCAA 406

QY 421 AGTTGGTCTCACATTTCACTCTCGAGGATCTCGCCAGCGGGGTCTCCCGAGAGACTTCGG 480

DB 405 AGTCGGCCTCACATTTCACTCTCGAGGATGTTTGGCCAGCGGTGCTTCTCTGAGGACTTTGG 346

Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Clas: sheared ends.

FEATURES
source

Location/Qualifiers
1..816
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMWBMA0639G14"
/clone_lib="ZM_0.7.1.5_KB"
/note="Vector: pBCKS-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 34.7%; Score 304.4; DB 9; Length 816;
Best Local Similarity 99.7%; Pred. No. 5.2e-79;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 571 GTACTTCATGCTAATGAGAAATTCATTCGATTGGCTTCTTTGATTTTCAGAAAG 630
Db 1 GTACTTCATGCTAATGAGAAATTCATTCGATTGGCTTCTTTGATTTTCAGAAAG 60
QY 631 TGTATTAGTAGTTTCAACAAAATAATAGCTCCATATTCGCTCTATATCCCGTATTTGAAA 690
Db 61 TGTATTAGTAGTTTCAACAAAATAATAGCTCCATATTCGCTCTATATCCCGTATTTGAAA 120
QY 691 TTCTAAGCCGTTTCTGATTACTGCTTACACAGAAAGTTTGTCTAGTTCCTACCTAC 750
Db 121 TTCTAAGCCGTTTCTGATTACTGCTTACACAGAAAGTTTGTCTAGTTCCTACCTAC 180
QY 751 GCTTTTTTTTGAAGTTTGTAGTGGAAACATCTTTGTTTCAACGTTTGGGAGGTGTAGGC 810
Db 181 GCTTTTTTTTGAAGTTTGTAGTGGAAACATCTTTGTTTCAACGTTTGGGAGGTGTAGGC 240
QY 811 CAGTAATCTGCAAGAAAGGAATATTTCCCTTGAGCAACATTTGTTTGTGATCCTT 870
Db 241 CAGTAATCTGCAAGAAAGGAATATTTCCCTTGAGCAACATTTGTTTGTGATCCTT 300
QY 871 GAAAAA 876
Db 301 GAACAA 306

RESULT 11
CB674853

LOCUS

CB674853 751 bp mRNA linear EST 09-APR-2003
OSJNEA10C10.f OSJNEE Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEE10C10.5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 Row: C Column: 10
Seq primer: gta aac cga cgg cca gtcg.
Location/Qualifiers
1..751

FEATURES
source

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEE10C10"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEE"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN

Query Match 33.3%; Score 291.6; DB 6; Length 751;
Best Local Similarity 74.9%; Pred. No. 3.3e-75;
Matches 394; Conservative 0; Mismatches 124; Indels 8; Gaps 2;
QY 47 GGAAGCGAGGAGCGGAGGAGGAGCATGGTGCACGGGACGCTGGAAGTGTCTGCTCGTTGGG 106
Db 48 GGGCGCGCGGGGAGCTGGGGAAGATGGTGCAGGGGACGCTCGAGGTGTCTGCTCGTCGGA 107
QY 107 GCCAAGGGCTTCAGAACACCGATTACCTCTGTAAACATGGATCCGTATGCAATTCCTCAAG 166
Db 108 GCCAAGGGCTTCAGAACACCGATTACCTCTGTAAACATGGATCCGTATGCAATTCCTCAAG 167
QY 167 TGGCGTTTCAGGAGCAGAGAGAGCAGTATTGGCAACTTGGAAAGGAACTACCCCTGAGTGG 226
Db 168 TGGCGCTCGCAGGAGCAGAGAGCAGCGTTGCGTCAAGTTAAGGATCTGACCTCGAATGG 227
QY 227 AATGAAACCTTTATCTTCACTGTGTCTGACCGGACCAACAGACTTGGTAAATCAAGCTTATG 286
Db 228 AAGCAAACTTTATGTTACGCGTCACTCAACCGCTACAGAGCTCATCATCAAGTTGATG 287
QY 287 GACAGTGATACAGGACAGCAGATGATCTTGTGTGGAAGCAACGATTCATTCGAGGCA 346
Db 288 GACAGTGATGAGCGGACGATGATGATTTGTTGGAGAGCAACAGATTTCTTTGGAAGCA 347
QY 347 GTGTATCTACTGAAAGGAGCATTCCACCAACACTCTATAATGTTGTGAAAGGTGAAAATAC 406
Db 348 ATCTATACAGAGAGAGCATACCCCACTGTTTATATGTTGTGAAGAGAGAGATAC 407
QY 407 TGGCGGGAATCAAAATTTGTTCTACATTCATCTCTGAGGATACCTGCCAGCGGGTCTC 466
Db 408 CGTGAGAAATCAAAAGTGGGCTGAGCTTCACTCCAGAGGATGATCGCATCGGGGTTTA 467
QY 467 CCAGAG--GACTTCGGTGGATGGAGCAATCATCTT-----AGACTAGATGCTTTAAG 518
Db 468 TCTGAGAGAGCATTTGTTGGATGGAAGCAGTCACTTTGAGGAGAGAGAGACTATTTGAT 527
QY 519 GTTGCAACAGAGCAGACAGCAATTCATGCGCTTGGAGGCTTCAGC 564
Db 528 GTCGCACTGCATCGCTATGTTAAGTCGTGCTGGNAGGCTGGNAC 573

RESULT 12

CA755886

LOCUS

DEFINITION

CA755886 622 bp mRNA linear EST 27-NOV-2002
BR030030000 PLATE_E11_85_086.ab1 OA Oryza sativa (japonica
cultivar-group) cDNA clone BR030030000 PLATE_E11_85_086.ab1 similar
to elicitor-responsive gene 3 [imported] - rice
gi|3603473|gb|AAC35866.1| (AF090698) elicitor-responsive gene-3
[Oryza sativa] [Oryza sativa (indica cultivar-group)]
gi|21998839|dbj|BAC06444.1| (AB060729) RPP16 [Oryza sativa]

```
ORIGIN
Query Match      42.0%; Score 367.8; DB 6; Length 371;
Best Local Similarity 99.5%; Pred. No. 5e-98;
Matches 369; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 146 GATCCGATGCAATTTCTCAAGTCCCGTTTCACAGGAGCAGAGCAGATTTGCAACTGGA 205
DB 1 GATCCGATGCAATTTCTCAAGTCCCGTTTCACAGGAGCAGAGCAGATTTGCAACTGGA 60
QY 206 AAGGAACTACCCCTGAGTGGAAATGAAAATTTATCTTCACTGTGTGACCGGCAACA 265
DB 61 AAGGAACTACCCCTGAGTGGAAATGAAAATTTATCTTCACTGTGTGACCGGCAACA 120
QY 266 GACTTCGTATCAAGCTTATGGACAGTGATACAGGACACAGCAGATCATCTTGTGGTGA 325
DB 121 GACTTCGTATCAAGCTTATGGACAGTGATACAGGACACAGCAGATCATCTTGTGGTGA 180
QY 326 GCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTCACCAACACTCTATAAT 385
DB 181 GCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTCACCAACACTCTATAAT 240
QY 386 GTTGTGAAAGGTGAAAATTAATCTCGGGGAAATCAAAAGTTGGTCTCATTCCTCTGAG 445
DB 241 GTTGTGAAAGGTGAAAATTAATCTCGGGGAAATCAAAAGTTGGTCTCATTCCTCTGAG 300
QY 446 GATACCTGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAGCAATCATCTTAGAC 505
DB 301 GATACCTGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGGAGCAATCATCTTAGAC 360
QY 506 TAGATGCTTTA 516
DB 361 TAGATGCTTTA 371

RESULT 9
BF482583 746 bp mRNA linear EST 06-DEC-2000
LOCUS WHE2301-2304_G04_G04ZS Wheat pre-anthesis spike cDNA library
DEFINITION Triticum aestivum cDNA clone WHE2301-2304_G04, mRNA sequence.
ACCESSION BF482583
VERSION BF482583.1 GI:11565973
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
AUTHORS Han, P.S., Heia, C.C., Kang, Y.Y., Iazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
FEATURES
source
1..746
Location/Qualifiers
/organism="Triticum aestivum"
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the T3 Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

CoT selected genomic DNA library"

ORIGIN

Query Match 49.4%; Score 432.8; DB 9; Length 977;
Best Local Similarity 98.4%; Pred. No. 2.9e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 433 ATTCATCTCCTGAGGATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 492
Db ATTCCTTTATGTAGGATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 71

QY 493 ATCATCTTAGCTAGATGCTTTAAGGTGCACAGAGCAGCAGCAATTCATCGCGTT 552
Db ATCATCTTAGAGCTAGATGCTTTAAGGTGCACAGAGCAGCAGCAATTCATCGCGTT 131

QY 553 GGAGCCTTCAGCGGTGAGTACTTCATCTAATGAGCAATTCATTCGATTTGGCTTCTTT 612
Db GGAGCCTTCAGCGGTGAGTACTTCATCTAATGAGCAATTCATTCGATTTGGCTTCTTT 191

QY 613 TGATTTGTTTCAGAGAGTGTATTAGTGTAGTTTCAACAAAAAATAGCTCCATATTGCTC 672
Db TGATTTGTTTCAGAGAGTGTATTAGTGTAGTTTCAACAAAAAATAGCTCCATATTGCTC 251

QY 673 TATATCCGTTATTGGAATTCCTAAGCGGCTTTGTGATTAATCTGCTTCAACAAAGAGTTT 732
Db TATATCCGTTATTGGAATTCCTAAGCGGCTTTGTGATTAATCTGCTTCAACAAAGAGTTT 311

QY 733 GCTTCTAGTCCCACTACGCTTTTGTGAGTTTGTGAGTGGAGCAATCTTTGTGTTCAAC 792
Db GCTTCTAGTCCCACTACGCTTTTGTGAGTTTGTGAGTGGAGCAATCTTTGTGTTCAAC 371

QY 793 GTTTGGGAGGTGTAGGCGAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACA 852
Db GTTTGGGAGGTGTAGGCGAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACA 431

QY 853 TTGTTTTTGTGATCCTTGA AAAA 876
Db TTGTTTTTGTGATCCTTGAACAA 455

RESULT 7
BZ538974 721 bp DNA linear GSS 16-DEC-2002
LOCUS OGAEC73TC ZM2 0.7 1.5 KB Zea mays genomic clone ZMBMa0040N01,
genomic survey sequence.
ACCESSION BZ538974
VERSION BZ538974.1 GI:27087410
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 721)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..721
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

/clone="ZMBMa0040N01"
/clone_lib="ZM2 0.7 1.5 KB"
/notes="vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 49.2%; Score 431.4; DB 8; Length 721;
Best Local Similarity 99.8%; Pred. No. 6.9e-117;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 444 AGGATATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATCATCTTAGA 503
Db AGGATATCTCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATCATCTTAGA 653

QY 504 GCTAGATGCTTTAAGGGTGACAGAGCAGCAGCAATTCATCGGCTTCGAGCCTTCAG 563
Db GCTAGATGCTTTAAGGGTGACAGAGCAGCAGCAATTCATCGGCTTCGAGCCTTCAG 593

QY 564 CCGTCGAGTACTTCATCTAATGAGCAATTCATTCGATTTGGCTTCTTTGATTTGTTTCA 623
Db CCGTCGAGTACTTCATCTAATGAGCAATTCATTCGATTTGGCTTCTTTGATTTGTTTCA 533

QY 624 GAAGAGTGTATTAGTGTAGTTTCAACAAAAAATAGCTCCATATTGCTCTATATCCGTA 683
Db GAAGAGTGTATTAGTGTAGTTTCAACAAAAAATAGCTCCATATTGCTCTATATCCGTA 473

QY 684 TTGGAATTTCTAAGCGGTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTG 743
Db TTGGAATTTCTAAGCGGTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTG 413

QY 744 CCATCTAGCTTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTG 803
Db CCATCTAGCTTTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTG 353

QY 804 TGAGGCGAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACAATGTTTTTGT 863
Db TGAGGCGAGTAATCTGCAAGAAAGAAATAATTTCCCTTGCAGCAACAATGTTTTTGT 293

QY 864 GATCCTTGA AAAA 876
Db GATCCTTGAACAA 280

RESULT 8
CD950747 371 bp mRNA linear EST 15-JUL-2003
LOCUS SAS_153 GeneTag2 Zea mays cDNA, mRNA sequence.
DEFINITION CD950747
ACCESSION CD950747
VERSION CD950747.1 GI:32798511
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 371)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..371
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

Db 365 ATCTCTTATAGGATACTCGCAGCGGGGTCTCCAGAGGACTTCGGTGATGGAAGCA 424
QY 493 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGGACAGGACAAATTCATGCGCTT 552
Db 425 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGGACAGGACAAATTCATGCGCTT 484
QY 553 GGAGCCTTCAGCGCTCGAGTACTTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 612
Db 485 GGAGCCTTCAGCGCTCGAGTACTTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 544
QY 613 TGATTTGTTTCAAGAGAGTGTATTAATAGTGTAGTTTCAACAAAAATAGCTCCATATTTGCTC 672
Db 545 TGATTTGTTTCAAGAGAGTGTATTAATAGTGTAGTTTCAACAAAAATAGCTCCATATTTGCTC 604
QY 673 TATATCCCGTATTTGGAATTTCTAAGCCGTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 732
Db 605 TATATCCCGTATTTGGAATTTCTAAGCCGTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 664
QY 733 GCTTCTAGTTCCCACTACGCTTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 792
Db 665 GCTTCTAGTTCCCACTACGCTTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 724
QY 793 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACA 852
Db 725 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACA 784
QY 853 TTGTTTTTTTGTGATCTTGGAAAA 876
Db 785 TTGTTTTTTTGTGATCTTGGAAAA 808

RESULT 5
CG372852
LOCUS
DEFINITION
CG372852
CG372852.1 GI:34290119
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 896)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG1DS04TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .896
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 49.4%; Score 432.8; DB 9; Length 896;

Best Local Similarity 98.4%; Pred. No. 2.8e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 433 ATCTACTCTTAGGATACTCGCAGCGGGGTCTCCAGAGGACTTCGGTGATGGAAGCA 492
Db 60 ATCTCTTATAGTAGGATACTCGCAGCGGGGTCTCCAGAGGACTTCGGTGATGGAAGCA 119
QY 493 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGGACAGGACAAATTCATGCGCTT 552
Db 120 ATCATCTTAGAGCTAGATGCTTTAAAGGGTGCACAGAGGACAGGACAAATTCATGCGCTT 179
QY 553 GGAGCCTTCAGCGCTCGAGTACTTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 612
Db 180 GGAGCCTTCAGCGCTCGAGTACTTTCATGCTAAATGCAGAAATTCATTCGATTTGGCTTCTTT 239
QY 613 TGATTTGTTTCAAGAGAGTGTATTAATAGTGTAGTTTCAACAAAAATAGCTCCATATTTGCTC 672
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QY 673 TATATCCCGTATTTGGAATTTCTAAGCCGTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 732
Db 300 TATATCCCGTATTTGGAATTTCTAAGCCGTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 359
QY 733 GCTTCTAGTTCCCACTACGCTTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 792
Db 360 GCTTCTAGTTCCCACTACGCTTTTGTGATTTAGTGGAAATCTTTGTTGTTCAAC 419
QY 793 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACA 852
Db 420 GTTTGGGAGGTGTAGCCAGTAAATCTGCAAGAAAGGAATATTTCCCTTGCAGCAACA 479
QY 853 TTGTTTTTTTGTGATCTTGGAAAA 876
Db 480 TTGTTTTTTTGTGATCTTGGAAAA 503

RESULT 6
CG171937
LOCUS
DEFINITION
CG171937
CG171937.1 GI:34062735
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 977)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFKS52TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .977
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high

FEATURES
source

FEATURES
source
1. .977
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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QY 597 TCGATTGGCTTCCTTTGATGTTTCAGAAAGAGTGTATTAGTGAAGTTTCAACAAAAA 656
Db 169 TCGATTGGCTTCCTTTGATGTTTCAGAAAGAGTGTATTAGTGAAGTTTCAACAAAAA 110
QY 657 TAGCTCCATATGCTCTATATCCCGTATTCGAAATCTTAAGCGCGTTTGTGATTACTGCT 716
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QY 717 TACAACAAGAGTTTGTCTTCTAGTCCCACTA 749
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RESULT 3
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LOCUS 660058D08.x2 660 - Mixed stages of anther and pollen Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AW519994
VERSION AW519994.1 GI:7162372
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 534)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 660058 row: D column: 08.
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location/Qualifiers
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/mol_type="mRNA"
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/notes="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
Site_2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amie Franklin."

ORIGIN
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Best Local Similarity 99.4%; Pred. No. 7.3e-143;
Matches 531; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 316 TGTGTGGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCAAC 375
Db 534 TGTGTGGAAGCAACGATTCATTTGGAAGCAGTGTATCTGAAAGGAGCATTTCCACCATC 475

QY 376 ACTCTATATGTTGGAAGTGAAATACTCGCGGGAATCAAGTGTGCTTCACATT 435
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QY 436 CACTCTCTGAGGATACCTGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATC 495
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Db 414 CACTCTCTGAGGATACCTGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCAATC 355
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QY 616 TTGTTTTCAGAAAGTGTATTAGTGAAGTTTCAACAAAAAATAGCTCCATATTCGCTCTAT 675
Db 234 TTGTTTTCAGAAAGTGTATTAGTGAAGTTTCAACAAAAAATAGCTCCATATTCGCTCTAT 175
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Db 174 ATCCCGTATTTGAAAATTCCTAAGCCGTTTGTGATTAAGTCTTACACAGAAAGTTTGGCT 115
QY 736 TCTAGTTCCCACTAGCSC--TTTTTTGAAGTTTGTAGTGGAAACATCTTTGTGTTCAACG 793
Db 114 TCTAGTTCCCACTAGCCTTTTGTGAAGTTTGTAGTGGAAACATCTTTGTGTTCAACG 55
QY 794 TTTGGGAGGTGTAGGCCAGTAAATCTGCAAGAAAGAAATAATTTCCCTTGCAG 847
Db 54 TTTGGGAGGTGTAGGCCAGTAAATCTGCAAGAAAGAAATAATTTCCCTTGCAG 1

RESULT 4
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LOCUS OG0GP83TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBma0713N22,
DEFINITION genomic survey sequence.
ACCESSION CG280271
VERSION CG280271.1 GI:34194390
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 860)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG0GP83TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
source
location/Qualifiers
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/clone="ZMMBma0713N22"
/clone_lib="ZM 0.7 1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 49.4%; Score 432.8; DB 9; Length 860;
Best Local Similarity 98.4%; Pred. No. 2.8e-117;
Matches 437; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 433 ATTCACTCTCTGAGGATACCTGCCAGCGGGGTCTCCAGAGGACTTCGGTGGATGGAAGCA 492
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Best Local Similarity 100.0%; Pred. No. 2.8e-247;
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 GTTCGTTCCAGCCAGGACAGCAGGCGCTTGTGAGGAGAGCGAGCGGAGGAG 67
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Db 274 GACATGGTGACGGGACGCTGGAAGTGTCTCTGTTGGGCGCCAGGCGCTTCGAGAACACC 333
QY 128 GATTACCTCTGTAACATGATGATGCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 187
Db 334 GATTACCTCTGTAACATGATGATGCGTATGCAATTTCTCAAGTGCCTTACAGGAGCAGAAG 393
QY 188 AGCAGTATTGCACTGGAAGGAGCACTACCCCTGAGTGGAAATGGAATTTATCTTCACT 247
Db 394 AGCAGTATTGCACTGGAAGGAGCACTACCCCTGAGTGGAAATGGAATTTATCTTCACT 453
QY 248 GTCTCTGACCGGACAAACAGACTTGGTAAATCAAGCTTATGACAGTGTATACAGGACAGCA 307
Db 454 GTCTCTGACCGGACAAACAGACTTGGTAAATCAAGCTTATGACAGTGTATACAGGACAGCA 513
QY 308 GATGACTTTTGGTGAAGCAACAGATTCCATTGGAAGCAGTGTATATGAAAGGAGCAATT 367
Db 514 GATGACTTTTGGTGAAGCAACAGATTCCATTGGAAGCAGTGTATATGAAAGGAGCAATT 573
QY 368 CCACCAACACTCTAATGTTGGAAGTGAAGAAATACCTCGGGGAAATCAAGTTGGT 427
Db 574 CCACCAACACTCTAATGTTGGAAGTGAAGAAATACCTCGGGGAAATCAAGTTGGT 633
QY 428 CTCACATTCACTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGG 487
Db 634 CTCACATTCACTCTGAGGATCTCGCCAGCGGGTCTCCAGAGGACTTCGGTGGATGG 693
QY 488 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCCAGAGCAGCAGGACAAATTCATG 547
Db 694 AAGCAATCATCTTAGAGCTAGATGCTTTAAGGGTGCCAGAGCAGCAGGACAAATTCATG 753
QY 548 CGCTTGGGCGCTTCAGCGCTGAGTACTCATGCTAATGCAAGATTCATTGCTTTGGCT 607
Db 754 CGCTTGGGCGCTTCAGCGCTGAGTACTCATGCTAATGCAAGATTCATTGCTTTGGCT 813
QY 608 TCTTTTGATTGTTTCAGAGAAAGTGTATTAGTGAGTTTCAACAAAAATAGCTCCATAT 667
Db 814 TCTTTTGATTGTTTCAGAGAAAGTGTATTAGTGAGTTTCAACAAAAATAGCTCCATAT 873
QY 668 TGCTCTATATCCCGTATTGGAATTTCTAAGGCGGTTTGTGATTTACTGTTTACAAAGAA 727
Db 874 TGCTCTATATCCCGTATTGGAATTTCTAAGGCGGTTTGTGATTTACTGTTTACAAAGAA 933
QY 728 GTTTTGTCTTAGTCTCCACTAGCTTTTGTGAGTTTGTGAGTGGAAATCTTTTGTGT 787
Db 934 GTTTTGTCTTAGTCTCCACTAGCTTTTGTGAGTTTGTGAGTGGAAATCTTTTGTGT 993
QY 788 TCAACGTTTGGGAGGTGTAGGCGAGTAACTACTGCAAGAAAGGAAATAATTTCCCTTGCAG 847
Db 994 TCAACGTTTGGGAGGTGTAGGCGAGTAACTACTGCAAGAAAGGAAATAATTTCCCTTGCAG 1053
QY 848 CAACATGTTTGTGATCTCTTGAAGAA 876
Db 1054 CAACATGTTTGTGATCTCTTGAAGAA 1082
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RESULT 2
BG842875/c
LOCUS
DEFINITION
EST 29-MAY-2001
MEST41-A12.T3 ISUM4-TN Zea mays cDNA clone MEST41-A12 3', mRNA
sequence.
BG842875
ACCESSION
BG842875.2 GI:14244937
VERSION
EST.
KEYWORDS
Zea mays
SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14209197.
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

PCR Primers

FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..589

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="MEST41-A12"

/tissue_type="Seedling and silk"

/lab_host="DH10B"

/clone_lib="ISUM4-TN"

/note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AATCGAAGATTCGCGCGCAGGAATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

FEATURES

source

ORIGIN

Query Match 65.0%; Score 569.8; DB 4; Length 589;
Best Local Similarity 99.7%; Pred. No. 3.6e-158;
Matches 571; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 177 AGGACGAGAGGAGCAGTATTGCAACTGGAAAGGAACTACCCCTGAGTGGAAATGAAACT 236
Db 589 AGGACGAGAGGAGCAGTATTGCAACTGGAAAGGAACTACCCCTGAGTGGAAATGAAACT 530
QY 237 TTATCTTCACTGTGTGCTGACCGGACCAACAGACTTGGTAATCAAGCTTATGGACAGTGATA 296
Db 529 TTATCTTCACTGTGTGCTGACCGGACCAACAGACTTGGTAATCAAGCTTATGGACAGTGATA 470
QY 297 CAGGACAGCAGATGACATTTTGTGGAAGCAACGATTCATTCCTGGAAGCAGTGTATCTG 356
Db 469 CAGGACAGCAGATGACATTTTGTGGAAGCAACGATTCATTCCTGGAAGCAGTGTATCTG 410
QY 357 AAAGGAGCATTCACCAACACTCTATATGTTGTAAGGTCGAAAGGTCGAAAGTACTCGGGGAAA 416
Db 409 AAAGGAGCATTCACCAACACTCTATATGTTGTAAGGTCGAAAGGTCGAAAGTACTCGGGGAAA 350
QY 417 TCAAGTGTGCTCATTCTCCTGAGGATACCTCGCCAGCGGGGTCTCCAGAGGACT 476
Db 349 TCAAGTGTGCTCATTCTCCTGAGGATACCTCGCCAGCGGGGTCTCCAGAGGACT 290
QY 477 TCGGTGGATGGAAGCAATCATCTTAGAGCTAGATGCTTTAAGGTGTCACAGACACAGC 536
Db 289 TCGGTGGATGGAAGCAATCATCTTAGATCTAGATGCTTTAAGGTGTCACAGACACAGC 230

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 06:21:19 ; Search time 3407 seconds
(without alignments)
9369.300 Million cell updates/sec

Title: US-09-913-569b-5
Perfect score: 876
Sequence: 1 gcacgagttcttcacgcc.....ttttgtgaccttgaaaaa 876

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	569.8	65.0	589	4	BG842875	BG842875 MEST41-A1
C 3	518.4	59.2	534	2	AW513994	AW513994 660058D08
4	432.8	49.4	860	9	C280271	C280271 OGGP83TH
5	432.8	49.4	866	9	C372852	C372852 OGD504TH
6	432.8	49.4	977	9	CG171937	CG171937 PUFK52TB
C 7	431.4	49.2	721	8	B2538974	B2538974 OGAEC73TC
8	367.8	42.0	371	6	CD950747	CD950747 SAS 153 G
9	335.8	38.3	746	2	BF482583	BF482583 WHE2301-2
10	304.4	34.7	816	9	CG237557	CG237557 OGYBD43TH
11	291.6	33.3	751	6	CB674853	CB674853 OSJNE10C
12	289.4	33.0	622	6	CA755886	CA755886 BRO300300
C 13	285	32.5	705	6	CA759891	CA759891 BRO60013A
14	284.2	32.4	540	6	CF335095	CF335095 JMT--04-K
15	279.4	31.9	676	7	D23846	D23846 RICR0374A R
16	277	31.6	698	5	BQ294856	BQ294856 WHE2855 B
17	277	31.6	704	7	CN012865	CN012865 WHE3953 H
18	276.2	31.5	595	5	BQ246171	BQ246171 TAB15015C
19	276.2	31.5	705	1	AU085943	AU085943
C 20	275.6	31.5	686	6	CB674854	CB674854 OSJNE10C
21	275.4	31.4	694	6	CD937116	CD937116 OV.106A24
22	275	31.4	453	1	AU223390	AU223390
23	273.8	31.3	618	6	CA497973	CA497973 WHE3236 F
24	273.6	31.2	508	4	BJ223340	BJ223340

25	271.8	31.0	607	5	BU984956	BU984956 HF05K17r
26	271.8	31.0	626	5	BQ459983	BQ459983 HA07111r
27	271.8	31.0	654	1	AJ432364	AJ432364 AJ432364
C 28	271.8	31.0	1114	7	CK166470	CK166470 FGAS05061
29	271	30.9	526	1	AL808244	AL808244 AL808244
30	270.2	30.8	608	4	BJ464274	BJ464274 BJ464274
31	270	30.8	582	6	CA018551	CA018551 HV08P06r
32	269.8	30.8	539	5	BQ765305	BQ765305 EBR003 SQ
33	269.6	30.8	547	6	CD055817	CD055817 HO10F09S
34	269.6	30.8	549	6	CA018844	CA018844 HV09N05r
C 35	269.6	30.8	671	4	BM371209	BM371209 EBR004 SQ
36	269	30.7	678	4	BJ466724	BJ466724 BJ466724
37	269	30.7	698	2	BF263276	BF263276 HV CE8000
38	269	30.7	890	2	BE216340	BE216340 HV_CEB001
39	267	30.5	645	2	BE445264	BE445264 WHE1133 A
C 40	267	30.5	687	4	BJ264621	BJ264621
41	267	30.5	687	6	CD899012	CD899012 GI74.110M
C 42	267	30.5	706	4	BJ308874	BJ308874 BJ308874
43	266.6	30.4	495	2	BE443195	BE443195 WHE1109 C
44	266.2	30.4	560	2	BE446350	BE446350 WHE1455_D
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ALIGNMENTS

RESULT 1	AY106647	Zea mays	1082 bp	mRNA	linear	HTC 16-OCT-2002
LOCUS	AY106647	Zea mays	PC0065540	mRNA sequence.		
DEFINITION	AY106647	Zea mays	PC0065540	mRNA sequence.		
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VERSION	AY106647.1	GI:21209725				
KEYWORDS	HTC.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE						
AUTHORS	Hailey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitgitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1082)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.					
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	/db_xref="taxon:4577"					
	/clone_lib="Maize Mapping Project/DuPont Consensus Library"					
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"					
ORIGIN						
Query Match	99.2%; Score 869; DB 3; Length 1082;					